



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2017 – 10:26 PM EDT

PDB ID : 3MJ4
Title : Crystal structure of UDP-galactopyranose mutase in complex with phosphate analog of UDP-galactopyranose
Authors : Karunan Partha, S.; Sadeghi-Khomami, A.; Slowski, K.; Kotake, T.; Thomas, N.R.; Jakeman, D.L.; Sanders, D.A.R.
Deposited on : unknown
Resolution : 2.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

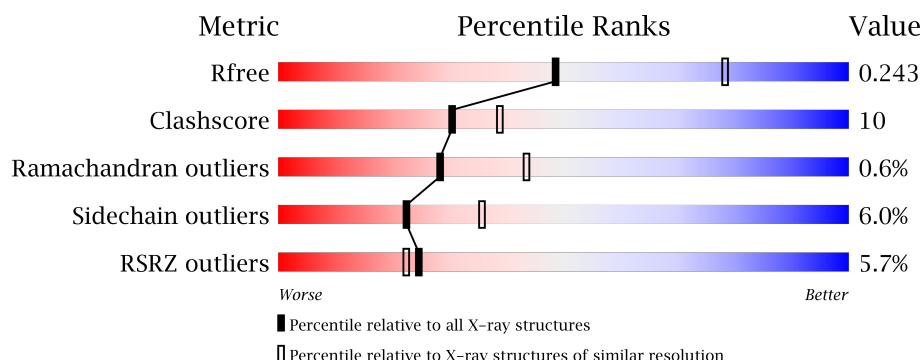
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3491 (2.70-2.62)
Clashscore	112137	1026 (2.68-2.64)
Ramachandran outliers	110173	1010 (2.68-2.64)
Sidechain outliers	110143	1010 (2.68-2.64)
RSRZ outliers	101464	3511 (2.70-2.62)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	397	<div> <div>2%</div> <div>70% 20% • 8%</div> </div>
1	B	397	<div> <div>11%</div> <div>66% 22% • 9%</div> </div>
1	C	397	<div> <div>3%</div> <div>70% 20% • 9%</div> </div>
1	D	397	<div> <div>11%</div> <div>68% 20% • 10%</div> </div>
1	E	397	<div> <div>8%</div> <div>66% 23% • 9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	397	
1	G	397	
1	H	397	
1	I	397	
1	J	397	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	398	-	-	-	X
4	GOL	B	398	-	-	-	X
4	GOL	C	398	-	-	-	X
4	GOL	E	398	-	-	-	X
4	GOL	F	398	-	-	-	X
4	GOL	F	400	-	-	-	X
4	GOL	G	399	-	-	-	X
4	GOL	H	398	-	-	-	X
4	GOL	I	398	-	-	-	X
4	GOL	J	399	-	-	-	X
4	GOL	J	400	-	-	-	X
6	XYL	F	399	-	-	-	X
6	XYL	I	401	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 31256 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called UDP-galactopyranose mutase.

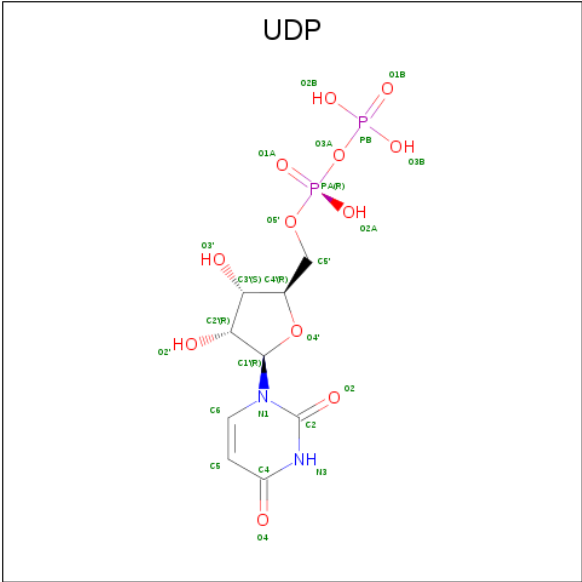
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	1	1	0
			2992	1909	521	554	8			
1	B	363	Total	C	N	O	S	1	0	0
			2969	1896	516	549	8			
1	C	363	Total	C	N	O	S	1	0	0
			2969	1896	516	549	8			
1	D	359	Total	C	N	O	S	0	0	0
			2943	1881	510	544	8			
1	E	361	Total	C	N	O	S	2	0	0
			2951	1885	512	546	8			
1	F	364	Total	C	N	O	S	1	1	0
			2984	1906	520	550	8			
1	G	363	Total	C	N	O	S	1	0	0
			2966	1894	515	549	8			
1	H	364	Total	C	N	O	S	0	0	0
			2975	1899	517	551	8			
1	I	364	Total	C	N	O	S	1	0	0
			2975	1899	516	552	8			
1	J	363	Total	C	N	O	S	2	0	0
			2966	1894	515	549	8			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	D	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	E	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	F	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	G	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	H	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	I	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	J	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: $\text{C}_9\text{H}_{14}\text{N}_2\text{O}_{12}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	C	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	E	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	F	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	G	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	H	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	I	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
3	J	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



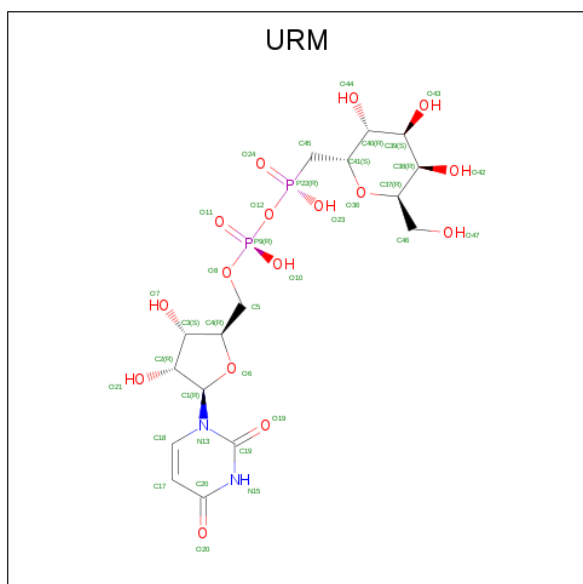
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

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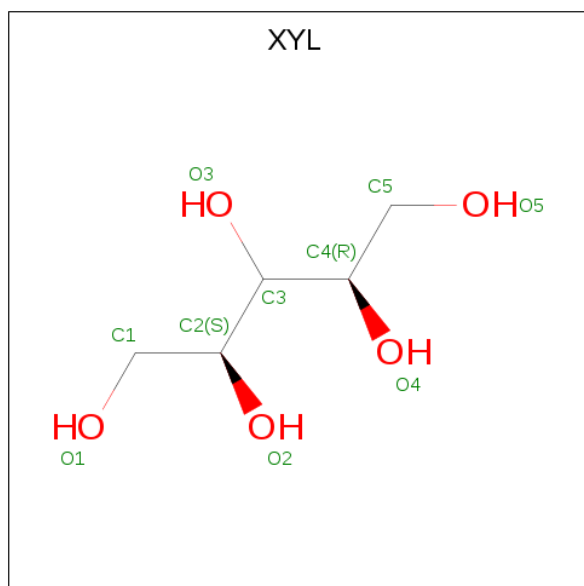
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is (((2S,3R,4S,5R,6R)-3,4,5-trihydroxy-6-(hydroxymethyl)tetrahydro-2H-pyran-2-yl)methyl)phosphonic (((2R,3S,4R,5R)-5-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)-3,4-dihydroxytetrahydrofuran-2-yl)methyl phosphoric) anhydride (three-letter code: URM) (formula: $C_{16}H_{26}N_2O_{16}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	N	O	P	0	0
			36	16	2	16	2		

- Molecule 6 is D-XYLITOL (three-letter code: XYL) (formula: $C_5H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	F	1	Total	C	O	0	0
			10	5	5		
6	I	1	Total	C	O	0	0
			10	5	5		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	89	Total	O	0	0
			89	89		
7	B	68	Total	O	0	0
			68	68		
7	C	60	Total	O	0	0
			60	60		
7	D	46	Total	O	0	0
			46	46		
7	E	51	Total	O	0	0
			51	51		
7	F	60	Total	O	0	0
			60	60		
7	G	53	Total	O	0	0
			53	53		

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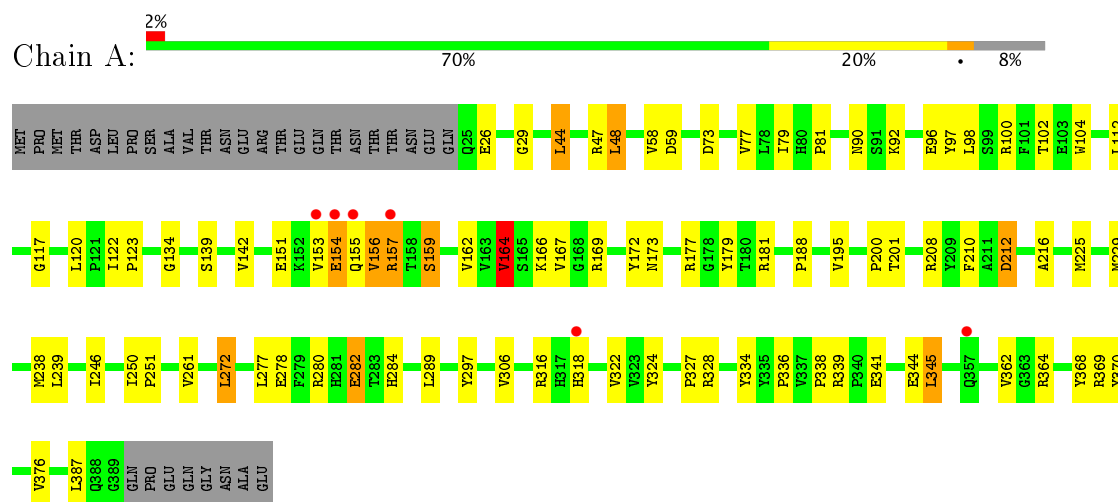
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	75	Total 75	O 75	0	0
7	I	65	Total 65	O 65	0	0
7	J	46	Total 46	O 46	0	0

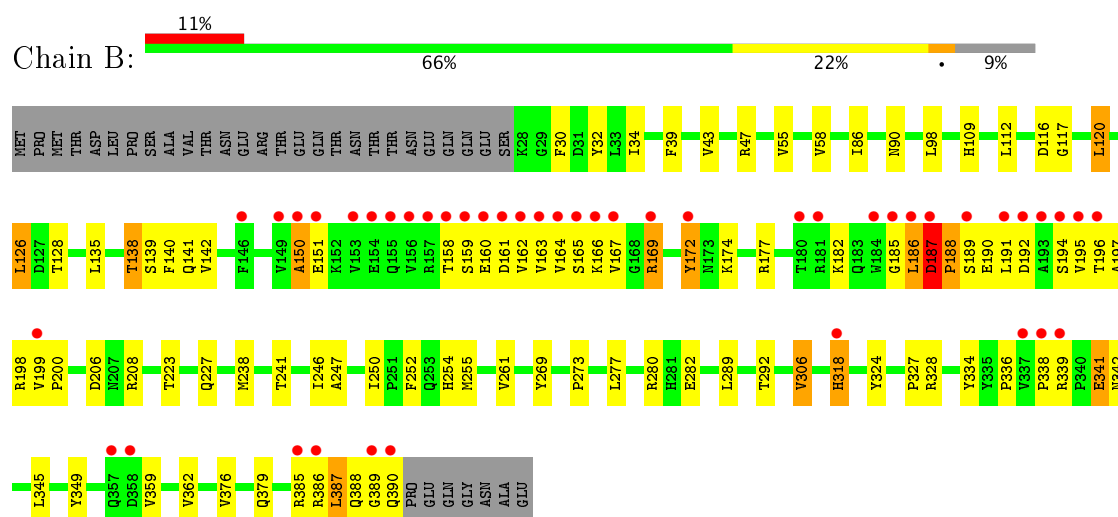
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: UDP-galactopyranose mutase

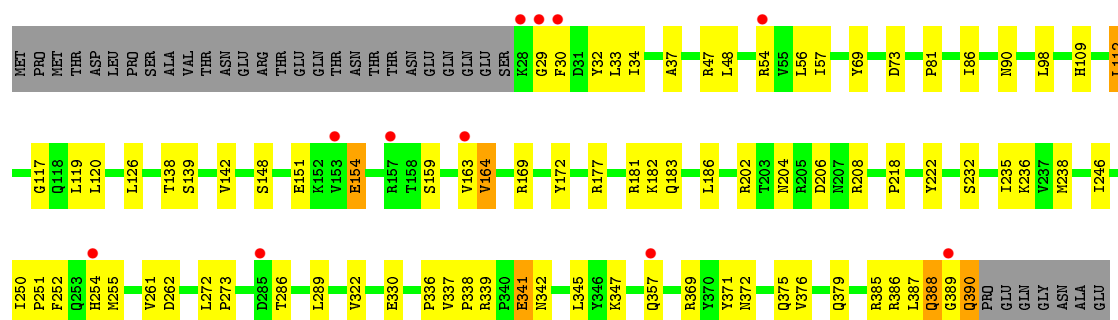


• Molecule 1: UDP-galactopyranose mutase

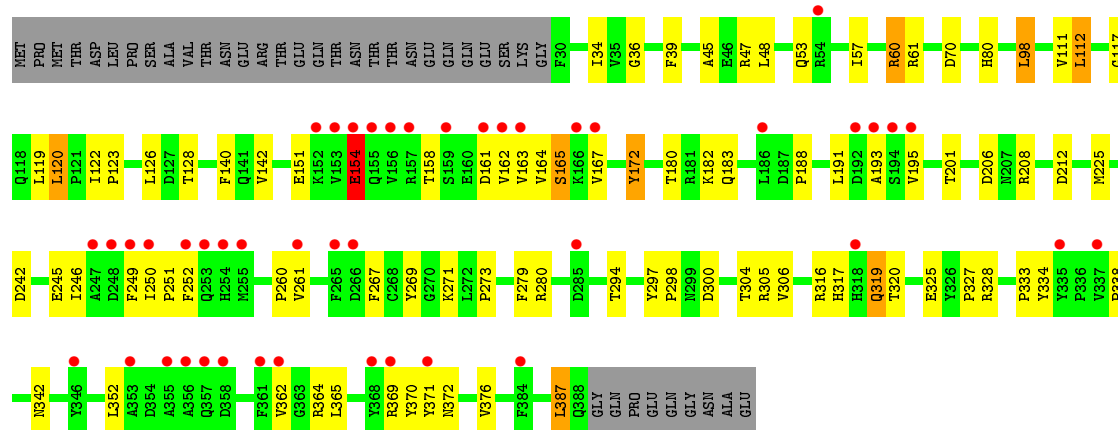


• Molecule 1: UDP-galactopyranose mutase

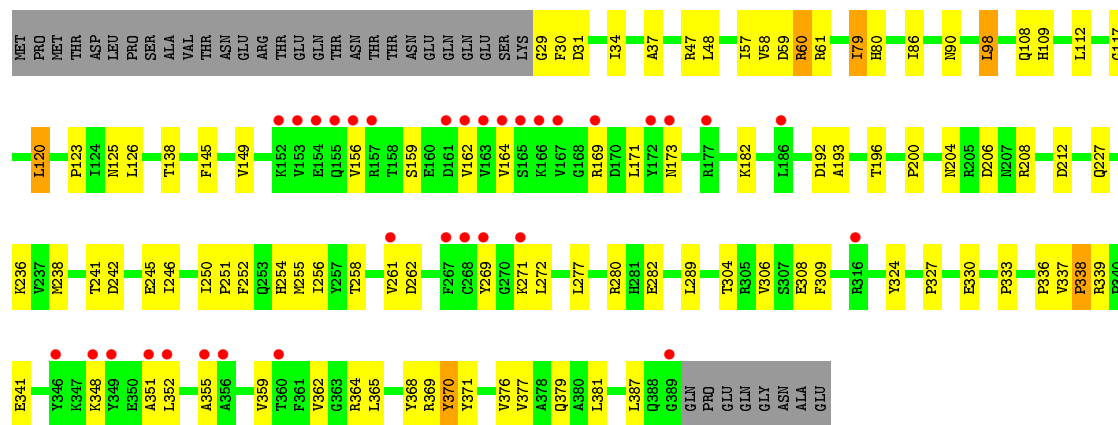




• Molecule 1: UDP-galactopyranose mutase

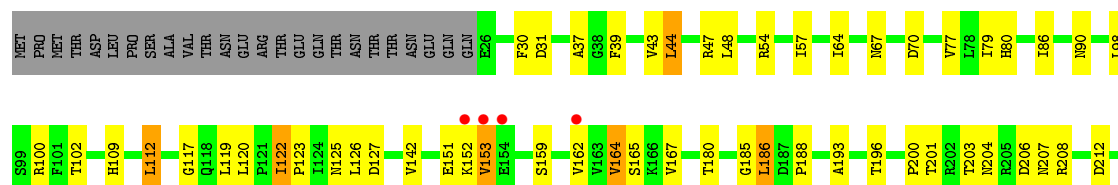


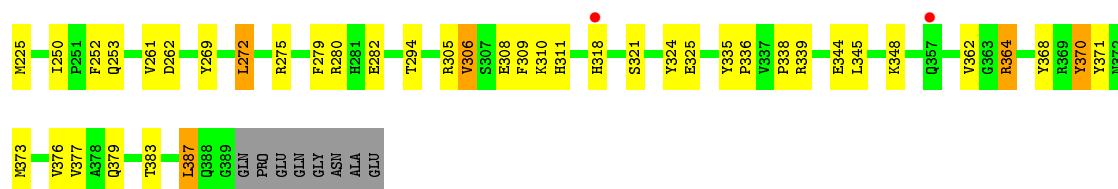
• Molecule 1: UDP-galactopyranose mutase



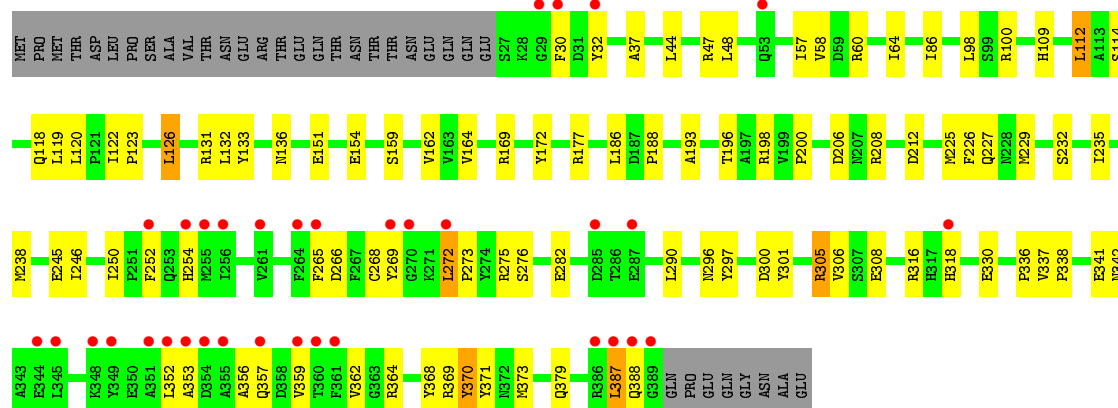
• Molecule 1: UDP-galactopyranose mutase







• Molecule 1: UDP-galactopyranose mutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.15Å 175.72Å 223.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.54 – 2.65 44.54 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.54-2.65) 99.5 (44.54-2.65)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.65Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.207 , 0.262 0.186 , 0.243	Depositor DCC
R_{free} test set	7672 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.417	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	31256	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, UDP, XYL, FAD, URM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.50	0/3079	0.65	0/4185
1	B	0.46	0/3053	0.62	0/4151
1	C	0.45	0/3053	0.62	0/4151
1	D	0.41	0/3027	0.57	0/4118
1	E	0.39	0/3035	0.55	0/4128
1	F	0.44	0/3072	0.62	0/4177
1	G	0.44	0/3050	0.59	0/4147
1	H	0.46	0/3059	0.60	0/4159
1	I	0.47	0/3059	0.62	0/4159
1	J	0.43	0/3050	0.58	0/4147
All	All	0.45	0/30537	0.60	0/41522

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2992	0	2867	69	0
1	B	2969	0	2843	109	0
1	C	2969	0	2843	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2943	0	2816	65	0
1	E	2951	0	2822	66	0
1	F	2984	0	2863	52	0
1	G	2966	0	2840	60	0
1	H	2975	0	2848	44	0
1	I	2975	0	2846	70	0
1	J	2966	0	2840	64	0
2	A	53	0	31	2	0
2	B	53	0	31	1	0
2	C	53	0	31	1	0
2	D	53	0	31	5	0
2	E	53	0	31	3	0
2	F	53	0	31	0	0
2	G	53	0	31	1	0
2	H	53	0	31	0	0
2	I	53	0	31	3	0
2	J	53	0	31	1	0
3	A	25	0	11	1	0
3	B	25	0	11	4	0
3	C	25	0	11	0	0
3	E	21	0	11	0	0
3	F	25	0	11	0	0
3	G	25	0	11	1	0
3	H	25	0	11	0	0
3	I	21	0	11	0	0
3	J	25	0	11	1	0
4	A	18	0	24	1	0
4	B	6	0	8	2	0
4	C	12	0	16	2	0
4	D	12	0	16	1	0
4	E	24	0	32	2	0
4	F	12	0	16	2	0
4	G	18	0	24	0	0
4	H	12	0	16	2	0
4	I	24	0	32	5	0
4	J	12	0	16	0	0
5	D	36	0	24	1	0
6	F	10	0	11	0	0
6	I	10	0	12	1	0
7	A	89	0	0	3	0
7	B	68	0	0	2	0
7	C	60	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	46	0	0	3	0
7	E	51	0	0	0	0
7	F	60	0	0	1	0
7	G	53	0	0	1	0
7	H	75	0	0	0	0
7	I	65	0	0	2	0
7	J	46	0	0	3	0
All	All	31256	0	29084	624	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (624) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:388:GLN:HA	1:C:388:GLN:NE2	1.45	1.12
1:A:153:VAL:HA	1:A:154:GLU:HB3	1.31	1.11
1:C:388:GLN:HE21	1:C:388:GLN:CA	1.66	1.08
1:C:389:GLY:C	1:C:390:GLN:HG2	1.74	1.02
1:G:58:VAL:HG23	1:G:238:MET:HB3	1.41	0.99
1:A:153:VAL:HA	1:A:154:GLU:CB	1.94	0.98
1:C:388:GLN:HE21	1:C:388:GLN:HA	0.78	0.94
1:C:389:GLY:O	1:C:390:GLN:HG2	1.68	0.93
1:A:154:GLU:HG2	1:A:155:GLN:H	1.36	0.91
1:I:371:TYR:HE2	1:I:379:GLN:HE21	1.19	0.90
1:C:388:GLN:CA	1:C:388:GLN:NE2	2.30	0.89
1:B:194:SER:O	1:B:198:ARG:HG3	1.78	0.84
1:B:189:SER:HA	1:B:190:GLU:HB2	1.56	0.84
1:B:169:ARG:HB3	1:B:169:ARG:HH11	1.42	0.83
1:D:151:GLU:HB2	1:D:164:VAL:HG12	1.60	0.83
1:B:198:ARG:HG2	1:B:198:ARG:HH11	1.44	0.82
1:G:151:GLU:HB2	1:G:164:VAL:HG12	1.62	0.81
1:B:169:ARG:NH1	1:B:169:ARG:HB3	1.94	0.81
1:A:153:VAL:CA	1:A:154:GLU:HB3	2.08	0.81
1:B:187:ASP:CG	1:B:188:PRO:HD2	2.02	0.80
1:C:90:ASN:HD22	4:C:398:GOL:H2	1.44	0.80
1:F:167:VAL:CG1	1:F:201:THR:HG21	2.12	0.80
1:D:267:PHE:CD1	1:D:271:LYS:HG2	2.17	0.80
1:B:376:VAL:HG21	2:B:450:FAD:H5'2	1.63	0.79
1:B:192:ASP:OD1	1:B:194:SER:HB3	1.81	0.79
1:G:304:THR:HG23	1:G:305:ARG:HG2	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:389:GLY:O	1:C:390:GLN:CG	2.30	0.79
1:F:167:VAL:HG11	1:F:201:THR:HG21	1.66	0.78
1:J:246:ILE:HD12	1:J:250:ILE:HD12	1.66	0.78
1:D:162:VAL:HG23	1:D:193:ALA:HB1	1.63	0.78
1:C:117:GLY:HA2	1:J:208:ARG:HD2	1.66	0.77
1:A:92:LYS:HE2	1:A:96:GLU:OE2	1.85	0.77
1:C:262:ASP:HB3	1:C:272:LEU:HD12	1.65	0.76
1:I:371:TYR:HE2	1:I:379:GLN:NE2	1.81	0.76
1:E:162:VAL:CG2	1:E:193:ALA:HB1	2.15	0.76
1:J:151:GLU:HB2	1:J:164:VAL:HG12	1.67	0.76
1:D:162:VAL:CG2	1:D:193:ALA:HB1	2.16	0.75
1:A:239:LEU:HD23	7:A:523:HOH:O	1.85	0.75
1:B:159:SER:OG	1:B:195:VAL:HB	1.87	0.74
1:E:162:VAL:HG23	1:E:193:ALA:HB1	1.69	0.74
1:G:336:PRO:O	1:G:338:PRO:HD3	1.87	0.74
1:D:280:ARG:HB3	7:D:584:HOH:O	1.86	0.74
1:B:318:HIS:CE1	1:H:316:ARG:HD3	2.22	0.74
1:A:173:ASN:OD1	1:A:177:ARG:NE	2.21	0.73
1:B:161:ASP:H	1:B:164:VAL:HG23	1.53	0.73
1:C:177:ARG:NH1	1:C:181:ARG:HH12	1.87	0.73
1:B:318:HIS:CD2	1:B:318:HIS:H	2.05	0.72
1:E:37:ALA:HA	1:E:57:ILE:HD11	1.70	0.72
1:I:152:LYS:HA	7:I:629:HOH:O	1.90	0.71
1:B:187:ASP:CB	1:B:188:PRO:HD2	2.20	0.70
1:I:371:TYR:CE2	1:I:379:GLN:NE2	2.59	0.70
1:J:162:VAL:CG2	1:J:193:ALA:HB1	2.21	0.70
1:B:388:GLN:HB2	7:B:656:HOH:O	1.92	0.70
1:F:117:GLY:HA2	1:H:208:ARG:HD2	1.75	0.69
1:G:162:VAL:CG2	1:G:193:ALA:HB1	2.23	0.69
1:B:206:ASP:OD1	1:B:208:ARG:HD3	1.94	0.68
1:G:272:LEU:HD22	1:G:368:TYR:CE1	2.29	0.68
1:I:269:TYR:CE2	1:I:348:LYS:HB3	2.29	0.68
1:J:86:ILE:HG21	1:J:109:HIS:HB2	1.75	0.68
1:A:376:VAL:HG21	2:A:450:FAD:H5'2	1.76	0.67
1:D:48:LEU:HD12	1:D:53:GLN:HG3	1.77	0.67
1:E:255:MET:HB3	1:E:359:VAL:HG22	1.77	0.67
1:E:280:ARG:NH1	1:E:282:GLU:OE2	2.27	0.67
1:E:29:GLY:HA2	1:E:251:PRO:HG2	1.76	0.67
1:H:29:GLY:HA3	1:H:251:PRO:HB2	1.77	0.66
1:F:206:ASP:OD1	1:F:208:ARG:HD3	1.95	0.66
1:F:89:THR:HA	4:F:398:GOL:H11	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:64:ILE:HD12	1:J:226:PHE:HB3	1.76	0.66
1:B:30:PHE:O	1:B:252:PHE:HA	1.96	0.66
1:I:371:TYR:HB3	1:I:376:VAL:HG23	1.78	0.66
1:H:246:ILE:HB	1:H:250:ILE:HD12	1.77	0.66
1:D:208:ARG:HD2	1:I:117:GLY:HA2	1.78	0.66
1:E:90:ASN:HD22	4:E:398:GOL:H2	1.61	0.65
1:I:207:ASN:HD21	4:I:402:GOL:H2	1.59	0.65
1:C:90:ASN:ND2	4:C:398:GOL:H2	2.10	0.65
1:C:336:PRO:O	1:C:338:PRO:HD3	1.96	0.65
1:G:162:VAL:HG23	1:G:193:ALA:HB1	1.79	0.65
1:I:336:PRO:O	1:I:338:PRO:HD3	1.97	0.65
1:J:206:ASP:OD1	1:J:208:ARG:HD3	1.97	0.65
1:B:150:ALA:O	1:B:151:GLU:HG3	1.96	0.65
1:B:160:GLU:HG2	1:B:164:VAL:CG2	2.26	0.65
1:H:253:GLN:HA	1:H:253:GLN:HE21	1.62	0.65
1:B:138:THR:HG23	1:B:140:PHE:H	1.62	0.64
1:B:158:THR:HA	1:B:191:LEU:O	1.97	0.64
1:E:262:ASP:OD2	1:E:271:LYS:HD2	1.96	0.64
1:A:250:ILE:HG12	1:I:250:ILE:HD13	1.80	0.63
1:I:122:ILE:HA	1:I:123:PRO:C	2.19	0.63
1:D:167:VAL:CG1	1:D:201:THR:HG21	2.29	0.63
1:B:138:THR:HG22	1:B:141:GLN:H	1.64	0.62
1:D:34:ILE:HD12	1:D:45:ALA:HB2	1.81	0.62
1:E:246:ILE:HD13	1:E:250:ILE:HD12	1.80	0.62
1:A:246:ILE:HB	1:A:250:ILE:HD12	1.82	0.62
1:J:112:LEU:HG	1:J:119:LEU:HB3	1.82	0.62
1:J:296:ASN:HA	1:J:305:ARG:HB3	1.82	0.61
1:G:206:ASP:OD1	1:G:208:ARG:HD3	2.00	0.61
1:B:280:ARG:NH1	1:B:282:GLU:OE2	2.33	0.61
1:B:117:GLY:CA	1:C:208:ARG:HD2	2.30	0.61
1:F:131:ARG:HD2	7:F:603:HOH:O	2.00	0.61
1:D:297:TYR:HE1	1:D:306:VAL:HG23	1.64	0.61
1:A:155:GLN:HB2	1:A:157[B]:ARG:HG3	1.82	0.61
2:D:450:FAD:HM71	7:D:580:HOH:O	1.99	0.61
1:B:185:GLY:O	1:B:186:LEU:HB3	2.01	0.61
1:B:187:ASP:OD1	1:B:188:PRO:HD2	2.01	0.61
1:E:306:VAL:HG22	1:E:324:TYR:CD1	2.36	0.60
1:A:212:ASP:OD2	1:A:212:ASP:N	2.31	0.60
1:B:160:GLU:HG2	1:B:164:VAL:HG21	1.83	0.60
1:I:37:ALA:HA	1:I:57:ILE:HD11	1.82	0.60
1:B:163:VAL:HG23	1:B:164:VAL:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:304:THR:HG23	1:G:305:ARG:CG	2.31	0.60
1:I:39:PHE:O	1:I:43:VAL:HG23	2.02	0.60
1:D:249:PHE:HE2	1:J:250:ILE:HG23	1.67	0.60
1:C:30:PHE:O	1:C:252:PHE:HA	2.02	0.60
1:E:206:ASP:OD1	1:E:208:ARG:HD3	2.02	0.60
1:B:126:LEU:HD23	1:B:142:VAL:CG2	2.32	0.59
1:D:269:TYR:HE2	1:D:352:LEU:HD11	1.67	0.59
1:D:183:GLN:HE22	1:D:305:ARG:HH12	1.51	0.59
1:G:122:ILE:HD12	1:G:123:PRO:HA	1.84	0.59
1:G:58:VAL:HG23	1:G:238:MET:CB	2.25	0.59
1:B:164:VAL:HG22	1:B:172:TYR:CD1	2.37	0.59
1:D:376:VAL:HG21	2:D:450:FAD:H5'2	1.83	0.59
1:H:64:ILE:HD12	1:H:226:PHE:HB3	1.84	0.59
1:E:336:PRO:O	1:E:338:PRO:HD3	2.03	0.59
1:H:162:VAL:CG2	1:H:193:ALA:HB1	2.32	0.59
1:E:123:PRO:HB3	1:E:200:PRO:O	2.03	0.58
1:C:372:ASN:HB2	1:C:375:GLN:HG3	1.84	0.58
1:J:272:LEU:HD22	1:J:368:TYR:CE1	2.39	0.58
1:B:255:MET:HB3	1:B:359:VAL:HG22	1.86	0.58
1:A:92:LYS:HE2	1:A:96:GLU:CD	2.24	0.58
1:B:195:VAL:CG2	1:B:338:PRO:HG2	2.34	0.58
1:I:151:GLU:HB2	1:I:164:VAL:HG13	1.85	0.58
1:B:138:THR:O	1:B:142:VAL:HG23	2.04	0.57
1:B:198:ARG:NH1	1:B:198:ARG:HG2	2.15	0.57
1:G:29:GLY:HA3	1:G:251:PRO:HB2	1.85	0.57
1:G:272:LEU:HD22	1:G:368:TYR:CZ	2.39	0.57
1:D:208:ARG:HD2	1:I:117:GLY:CA	2.33	0.57
1:A:154:GLU:HG2	1:A:155:GLN:N	2.13	0.57
1:B:138:THR:OG1	1:G:135:LEU:HD23	2.04	0.57
1:J:297:TYR:HE1	1:J:306:VAL:HG23	1.69	0.57
1:D:163:VAL:HG12	1:D:172:TYR:HB2	1.86	0.57
1:F:262:ASP:HB3	1:F:272:LEU:HB2	1.87	0.57
1:J:369:ARG:HD3	1:J:371:TYR:CZ	2.39	0.57
1:B:117:GLY:HA3	1:C:208:ARG:HD2	1.85	0.57
1:B:339:ARG:HB3	1:B:341:GLU:OE2	2.05	0.57
1:C:177:ARG:HH11	1:C:181:ARG:HH12	1.52	0.57
1:C:37:ALA:HA	1:C:57:ILE:HD11	1.86	0.57
1:I:125:ASN:HB2	1:I:204:ASN:O	2.04	0.57
1:I:306:VAL:HG13	1:I:324:TYR:CD1	2.39	0.57
1:A:334:TYR:O	1:A:364:ARG:NH1	2.37	0.57
1:D:47:ARG:NE	1:D:47:ARG:HA	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:112:LEU:HG	1:G:119:LEU:HB3	1.87	0.57
1:I:67:ASN:HD21	2:I:450:FAD:C8M	2.17	0.57
1:A:284:HIS:CD2	1:A:289:LEU:HD22	2.40	0.56
1:D:151:GLU:HB2	1:D:164:VAL:CG1	2.34	0.56
1:F:327:PRO:O	1:F:328:ARG:HD3	2.04	0.56
1:F:192:ASP:HB2	1:F:338:PRO:O	2.05	0.56
1:I:269:TYR:CD2	1:I:348:LYS:HB3	2.40	0.56
1:B:47:ARG:HA	1:B:47:ARG:NE	2.19	0.56
1:H:336:PRO:O	1:H:338:PRO:HD3	2.05	0.56
1:D:370:TYR:HE1	2:D:450:FAD:H1'1	1.71	0.56
1:B:169:ARG:CB	1:B:169:ARG:HH11	2.14	0.56
1:D:269:TYR:CE2	1:D:352:LEU:HD11	2.41	0.56
1:D:195:VAL:CG2	1:D:338:PRO:HG2	2.36	0.56
1:J:131:ARG:HD2	7:J:432:HOH:O	2.06	0.56
1:J:272:LEU:HD22	1:J:368:TYR:CZ	2.40	0.56
1:C:289:LEU:HD23	1:C:322:VAL:HG11	1.87	0.56
1:D:297:TYR:HE1	1:D:306:VAL:CG2	2.19	0.56
1:A:122:ILE:HD12	1:A:123:PRO:HA	1.87	0.56
1:A:153:VAL:CA	1:A:154:GLU:CB	2.72	0.56
1:E:29:GLY:CA	1:E:251:PRO:HG2	2.36	0.56
1:C:117:GLY:CA	1:J:208:ARG:HD2	2.33	0.55
1:J:371:TYR:HE2	1:J:379:GLN:NE2	2.02	0.55
1:A:123:PRO:HB3	1:A:200:PRO:O	2.05	0.55
1:F:84:PRO:HD2	1:F:325:GLU:OE1	2.05	0.55
1:B:246:ILE:HB	1:B:250:ILE:HD12	1.89	0.55
1:E:79:ILE:HG12	1:E:80:HIS:N	2.21	0.55
1:I:280:ARG:NH1	1:I:282:GLU:OE2	2.39	0.55
1:I:308:GLU:HB3	1:I:311:HIS:HD2	1.70	0.55
1:J:126:LEU:O	1:J:126:LEU:HD22	2.05	0.55
1:B:196:THR:HG22	3:B:500:UDP:H1'	1.89	0.55
1:E:86:ILE:HD12	1:E:86:ILE:N	2.22	0.55
1:F:30:PHE:O	1:F:252:PHE:HA	2.07	0.55
1:F:336:PRO:O	1:F:338:PRO:HD3	2.05	0.55
1:J:151:GLU:OE2	1:J:164:VAL:HG11	2.07	0.55
1:H:151:GLU:HB2	1:H:164:VAL:CG1	2.36	0.55
1:D:364:ARG:HG3	1:D:365:LEU:HG	1.89	0.55
1:E:206:ASP:OD2	1:E:208:ARG:NH1	2.39	0.55
1:A:117:GLY:CA	1:G:208:ARG:HD2	2.37	0.55
1:C:151:GLU:HB2	1:C:164:VAL:HG13	1.88	0.54
1:A:316:ARG:HD3	1:I:318:HIS:CD2	2.42	0.54
1:B:362:VAL:HG23	1:B:379:GLN:HG2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:GLY:HA2	1:F:208:ARG:HD2	1.89	0.54
1:D:122:ILE:HA	1:D:123:PRO:C	2.28	0.54
1:A:153:VAL:HG13	1:A:154:GLU:HB3	1.90	0.54
1:B:158:THR:HG22	1:B:191:LEU:O	2.08	0.54
1:G:111:VAL:HG22	1:G:294:THR:HB	1.87	0.54
1:J:58:VAL:HG23	1:J:238:MET:HG2	1.90	0.54
1:C:232:SER:HB3	1:C:235:ILE:HG13	1.90	0.54
1:B:327:PRO:O	1:B:328:ARG:HD3	2.08	0.54
1:J:269:TYR:CZ	1:J:352:LEU:HD11	2.43	0.54
1:D:273:PRO:HG2	1:D:342:ASN:OD1	2.08	0.54
1:D:316:ARG:HD3	1:J:318:HIS:CD2	2.42	0.54
1:E:371:TYR:HE2	1:E:379:GLN:NE2	2.06	0.54
1:A:117:GLY:HA3	1:G:208:ARG:HD2	1.89	0.54
1:E:272:LEU:HD22	1:E:368:TYR:CZ	2.43	0.54
1:J:172:TYR:OH	1:J:188:PRO:HG2	2.07	0.54
1:D:195:VAL:HG23	1:D:338:PRO:HG2	1.89	0.53
1:B:159:SER:O	1:B:196:THR:OG1	2.19	0.53
1:B:186:LEU:O	1:B:187:ASP:CB	2.57	0.53
1:I:310:LYS:HG3	7:I:406:HOH:O	2.08	0.53
1:B:86:ILE:HG21	1:B:109:HIS:HB2	1.88	0.53
1:F:289:LEU:HD23	1:F:322:VAL:HG11	1.89	0.53
1:D:140:PHE:CD2	4:D:399:GOL:H2	2.43	0.53
1:D:70:ASP:HB3	1:D:80:HIS:HD2	1.72	0.53
1:E:60:ARG:HA	1:E:241:THR:H	1.73	0.53
1:B:208:ARG:HD2	1:G:117:GLY:CA	2.38	0.53
1:J:387:LEU:O	1:J:388:GLN:HG2	2.09	0.53
1:C:371:TYR:CE1	1:C:379:GLN:NE2	2.77	0.53
1:G:261:VAL:HG22	1:G:366:ALA:O	2.09	0.52
1:E:182:LYS:HG2	1:E:304:THR:HG22	1.91	0.52
1:J:159:SER:HB3	1:J:196:THR:HG23	1.91	0.52
1:A:153:VAL:CG1	1:A:154:GLU:HB3	2.39	0.52
1:B:172:TYR:OH	1:B:177:ARG:HG3	2.09	0.52
1:H:162:VAL:HG23	1:H:193:ALA:HB1	1.91	0.52
1:I:376:VAL:HG21	2:I:450:FAD:H5'2	1.91	0.52
1:A:139:SER:O	1:A:142:VAL:HG12	2.10	0.52
3:G:500:UDP:H5'1	3:G:500:UDP:O2B	2.09	0.52
1:I:151:GLU:HB2	1:I:164:VAL:CG1	2.39	0.52
1:C:151:GLU:HB2	1:C:164:VAL:CG1	2.40	0.52
1:J:47:ARG:HA	1:J:47:ARG:NE	2.25	0.52
1:A:272:LEU:HD22	1:A:368:TYR:CZ	2.45	0.52
1:D:316:ARG:HD3	1:J:318:HIS:NE2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:159:SER:HA	1:E:193:ALA:HA	1.91	0.51
1:A:250:ILE:HG12	1:I:250:ILE:CD1	2.40	0.51
1:B:238:MET:HE1	1:B:246:ILE:HG21	1.91	0.51
1:G:357:GLN:OE1	1:G:357:GLN:HA	2.08	0.51
1:A:167:VAL:CG1	1:A:201:THR:HG21	2.40	0.51
1:A:47:ARG:HA	1:A:47:ARG:NE	2.26	0.51
1:E:60:ARG:HD2	2:E:450:FAD:C4A	2.41	0.51
1:H:69:TYR:O	1:H:81:PRO:HD2	2.09	0.51
1:A:297:TYR:HE1	1:A:306:VAL:HG23	1.75	0.51
1:J:337:VAL:HB	1:J:342:ASN:HD22	1.75	0.51
1:A:172:TYR:OH	1:A:188:PRO:HG2	2.11	0.51
1:J:86:ILE:N	1:J:86:ILE:HD12	2.26	0.51
1:A:336:PRO:O	1:A:338:PRO:HD3	2.10	0.51
1:A:277:LEU:HD23	1:A:327:PRO:HA	1.92	0.50
1:B:186:LEU:O	1:B:187:ASP:HB2	2.09	0.50
1:C:246:ILE:HB	1:C:250:ILE:HD12	1.92	0.50
1:B:172:TYR:CE2	1:B:177:ARG:HD3	2.45	0.50
1:D:36:GLY:O	1:D:57:ILE:HD11	2.12	0.50
1:H:122:ILE:HA	1:H:123:PRO:C	2.31	0.50
1:C:139:SER:O	1:C:142:VAL:HG12	2.11	0.50
1:D:120:LEU:HB3	1:D:128:THR:HG23	1.93	0.50
1:B:39:PHE:O	1:B:43:VAL:HG23	2.12	0.50
1:E:162:VAL:HG21	1:E:193:ALA:HB1	1.90	0.50
1:F:117:GLY:CA	1:H:208:ARG:HD2	2.40	0.50
1:I:102:THR:HB	1:I:225:MET:HG3	1.93	0.50
1:H:180:THR:HB	1:H:188:PRO:HG3	1.94	0.50
1:B:199:VAL:HG22	3:B:500:UDP:O2A	2.11	0.50
1:C:376:VAL:HG21	2:C:450:FAD:H5'2	1.92	0.50
1:E:117:GLY:CA	1:I:208:ARG:HD2	2.42	0.50
1:F:262:ASP:OD1	1:F:263:ALA:N	2.44	0.50
1:J:275:ARG:HG3	1:J:276:SER:N	2.26	0.50
1:I:80:HIS:HB2	1:I:309:PHE:CE2	2.46	0.50
1:B:162:VAL:HG21	1:B:197:ALA:HB2	1.92	0.50
1:C:47:ARG:HA	1:C:47:ARG:NE	2.26	0.50
1:F:269:TYR:CE2	1:F:352:LEU:HD11	2.46	0.50
1:D:279:PHE:CD2	1:D:325:GLU:HG2	2.47	0.50
1:E:159:SER:HB3	1:E:196:THR:HG23	1.93	0.50
1:F:369:ARG:HD2	1:F:371:TYR:CZ	2.46	0.50
1:I:30:PHE:O	1:I:252:PHE:HA	2.11	0.50
1:F:272:LEU:HD22	1:F:368:TYR:CZ	2.47	0.49
1:I:294:THR:HG21	1:I:305:ARG:CZ	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:253:GLN:HA	1:I:253:GLN:NE2	2.27	0.49
1:J:30:PHE:O	1:J:252:PHE:HA	2.12	0.49
1:B:273:PRO:HG2	1:B:342:ASN:OD1	2.12	0.49
1:H:206:ASP:OD1	1:H:208:ARG:HD3	2.12	0.49
1:A:376:VAL:HG21	2:A:450:FAD:C5'	2.41	0.49
1:J:169:ARG:HD2	7:J:641:HOH:O	2.13	0.49
1:A:151:GLU:HB2	1:A:164:VAL:HG13	1.95	0.49
1:G:308:GLU:HG3	1:G:322:VAL:HG12	1.95	0.49
1:J:337:VAL:HB	1:J:342:ASN:ND2	2.28	0.49
1:J:269:TYR:OH	1:J:352:LEU:HD21	2.12	0.49
1:B:135:LEU:HD23	1:C:138:THR:HG21	1.93	0.49
1:B:336:PRO:O	1:B:338:PRO:HD3	2.12	0.49
1:C:151:GLU:OE2	1:C:169:ARG:NH2	2.45	0.49
1:E:145:PHE:O	1:E:149:VAL:HG22	2.12	0.49
1:G:111:VAL:HG12	1:G:122:ILE:CG2	2.42	0.49
1:J:58:VAL:HG23	1:J:238:MET:HB3	1.95	0.49
1:H:90:ASN:ND2	4:H:398:GOL:H2	2.28	0.49
1:H:97:TYR:HD2	1:H:98:LEU:HD13	1.77	0.49
1:J:275:ARG:HG3	1:J:276:SER:H	1.78	0.49
1:A:29:GLY:HA3	1:A:251:PRO:HB2	1.93	0.49
1:B:163:VAL:CG2	1:B:164:VAL:N	2.75	0.49
1:G:297:TYR:HE1	1:G:306:VAL:HG23	1.76	0.49
1:I:90:ASN:HD22	4:I:398:GOL:H32	1.78	0.49
1:A:90:ASN:HD22	4:A:398:GOL:H12	1.76	0.49
1:C:273:PRO:HG2	1:C:342:ASN:OD1	2.13	0.49
1:D:249:PHE:CE2	1:J:250:ILE:HG23	2.46	0.49
1:E:125:ASN:HB2	1:E:204:ASN:O	2.12	0.49
1:D:117:GLY:CA	1:F:208:ARG:HD2	2.42	0.49
1:G:162:VAL:HG21	1:G:193:ALA:HB1	1.94	0.49
1:G:167:VAL:HG12	1:G:201:THR:HG21	1.93	0.49
1:A:73:ASP:HB3	1:A:79:ILE:HD13	1.95	0.49
1:B:32:TYR:CD1	1:B:254:HIS:HB3	2.47	0.48
1:D:122:ILE:HG13	1:D:123:PRO:HA	1.95	0.48
1:E:371:TYR:CE2	1:E:379:GLN:NE2	2.80	0.48
1:I:90:ASN:HD22	4:I:398:GOL:C3	2.26	0.48
1:B:199:VAL:HG21	3:B:500:UDP:C6	2.48	0.48
1:B:90:ASN:ND2	4:B:398:GOL:H2	2.28	0.48
1:B:160:GLU:C	1:B:162:VAL:H	2.17	0.48
1:H:280:ARG:NH2	1:H:326:TYR:OH	2.46	0.48
1:I:212:ASP:OD1	4:I:398:GOL:H2	2.13	0.48
1:I:364:ARG:NH2	1:I:370:TYR:CD2	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:ARG:HD2	7:B:505:HOH:O	2.13	0.48
1:A:280:ARG:NH1	1:A:282:GLU:OE1	2.46	0.48
1:D:60:ARG:HD3	2:D:450:FAD:C5A	2.43	0.48
1:H:294:THR:HG21	1:H:305:ARG:HH11	1.79	0.48
1:B:47:ARG:HA	1:B:47:ARG:HE	1.77	0.48
1:G:58:VAL:HG22	1:G:241:THR:HB	1.95	0.48
1:J:132:LEU:HD23	1:J:133:TYR:CZ	2.48	0.48
1:A:327:PRO:O	1:A:328:ARG:HD3	2.13	0.48
1:E:86:ILE:HG21	1:E:109:HIS:HB2	1.94	0.48
1:E:369:ARG:HD2	1:E:371:TYR:CE2	2.48	0.48
1:H:67:ASN:HB3	1:H:85:HIS:NE2	2.29	0.48
1:B:199:VAL:HG21	3:B:500:UDP:H6	1.79	0.48
1:E:61:ARG:HG3	2:E:450:FAD:O2B	2.14	0.48
1:D:250:ILE:O	1:D:252:PHE:HD2	1.97	0.48
1:B:163:VAL:O	1:B:166:LYS:N	2.47	0.48
1:G:306:VAL:HG22	1:G:324:TYR:CD1	2.49	0.48
1:C:69:TYR:O	1:C:81:PRO:HD2	2.14	0.47
1:F:86:ILE:HG21	1:F:109:HIS:HB2	1.96	0.47
1:I:112:LEU:HG	1:I:119:LEU:HB3	1.95	0.47
1:I:77:VAL:HG11	1:I:321:SER:HB2	1.95	0.47
1:I:142:VAL:HG13	1:I:203:THR:HG22	1.95	0.47
1:B:138:THR:HG23	1:B:140:PHE:N	2.28	0.47
1:B:160:GLU:O	1:B:161:ASP:HB2	2.14	0.47
1:F:123:PRO:HB3	1:F:200:PRO:O	2.14	0.47
1:F:44:LEU:HD13	1:F:362:VAL:HG11	1.96	0.47
1:A:44:LEU:O	1:A:48:LEU:HB2	2.14	0.47
1:B:150:ALA:HB1	1:B:165:SER:O	2.14	0.47
1:C:33:LEU:HD23	1:C:255:MET:HE2	1.96	0.47
1:D:112:LEU:HG	1:D:119:LEU:HB3	1.96	0.47
1:J:122:ILE:HA	1:J:123:PRO:C	2.35	0.47
1:G:208:ARG:HB3	7:G:401:HOH:O	2.13	0.47
1:H:364:ARG:HG3	1:H:369:ARG:O	2.14	0.47
1:F:180:THR:HG23	1:F:184:TRP:CD1	2.50	0.47
1:G:70:ASP:OD1	1:G:222:TYR:N	2.48	0.47
1:D:182:LYS:HG2	1:D:304:THR:HG22	1.97	0.47
1:F:369:ARG:NH1	1:F:379:GLN:HE21	2.12	0.47
1:H:28:LYS:HE2	1:H:28:LYS:HA	1.96	0.47
1:I:253:GLN:HA	1:I:253:GLN:HE21	1.78	0.47
1:E:364:ARG:NH2	1:E:370:TYR:CD1	2.82	0.47
1:B:306:VAL:HG13	1:B:324:TYR:CD1	2.50	0.47
1:G:151:GLU:OE2	1:G:164:VAL:HG11	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:272:LEU:HD22	1:F:368:TYR:CE1	2.49	0.47
1:B:246:ILE:HD12	1:B:247:ALA:N	2.30	0.47
1:I:123:PRO:HB3	1:I:200:PRO:O	2.15	0.47
1:I:279:PHE:CE2	1:I:325:GLU:HG2	2.50	0.47
1:F:137:LEU:HA	1:F:141:GLN:OE1	2.15	0.46
1:G:44:LEU:HD13	1:G:256:ILE:HG21	1.96	0.46
1:H:90:ASN:HD22	4:H:398:GOL:H2	1.81	0.46
1:I:180:THR:HG21	1:I:188:PRO:HG3	1.98	0.46
1:B:195:VAL:HG23	1:B:338:PRO:HG2	1.96	0.46
1:B:318:HIS:N	1:B:318:HIS:CD2	2.80	0.46
1:D:161:ASP:O	1:D:165:SER:HB3	2.16	0.46
1:H:305:ARG:HD2	1:H:325:GLU:OE1	2.15	0.46
1:J:177:ARG:HD2	7:J:642:HOH:O	2.15	0.46
1:B:34:ILE:HD12	1:B:55:VAL:HG11	1.96	0.46
1:I:262:ASP:HB3	1:I:272:LEU:HB2	1.97	0.46
1:B:120:LEU:HB3	1:B:128:THR:HG23	1.96	0.46
1:B:385:ARG:HG2	1:B:390:GLN:OE1	2.16	0.46
1:C:86:ILE:HG21	1:C:109:HIS:HB2	1.98	0.46
1:D:327:PRO:O	1:D:328:ARG:HD3	2.16	0.46
1:J:364:ARG:NH2	1:J:370:TYR:HD1	2.14	0.46
1:E:208:ARG:HD2	1:H:117:GLY:CA	2.45	0.46
1:H:29:GLY:O	1:H:54:ARG:CZ	2.63	0.46
1:A:278:GLU:HG3	1:A:328:ARG:CG	2.46	0.46
1:F:277:LEU:HD23	1:F:327:PRO:HA	1.98	0.46
1:A:289:LEU:HD23	1:A:322:VAL:HG11	1.98	0.46
1:B:185:GLY:O	1:B:186:LEU:CB	2.63	0.46
1:E:30:PHE:O	1:E:252:PHE:HA	2.16	0.46
1:F:118:GLN:HB3	1:F:120:LEU:HD13	1.96	0.46
1:I:153:VAL:HG23	1:I:165:SER:HB3	1.97	0.46
1:D:111:VAL:HG22	1:D:294:THR:HB	1.96	0.46
1:D:39:PHE:CE2	1:D:225:MET:HE3	2.49	0.46
1:I:47:ARG:NH1	1:I:100:ARG:HH12	2.14	0.46
1:B:58:VAL:HG12	1:B:238:MET:HB3	1.97	0.46
1:C:163:VAL:HG12	1:C:172:TYR:HB2	1.97	0.46
1:D:206:ASP:OD1	1:D:208:ARG:HD3	2.16	0.46
1:E:236:LYS:HD3	1:E:236:LYS:HA	1.70	0.46
1:G:47:ARG:HA	1:G:47:ARG:NE	2.30	0.46
1:C:29:GLY:O	1:C:54:ARG:NH1	2.49	0.46
1:G:246:ILE:HB	1:G:250:ILE:HD12	1.96	0.46
1:I:185:GLY:O	1:I:186:LEU:HD13	2.16	0.46
1:A:272:LEU:HD13	1:A:368:TYR:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:389:GLY:O	1:C:390:GLN:CD	2.55	0.45
1:I:207:ASN:ND2	4:I:402:GOL:H2	2.30	0.45
1:J:225:MET:HG2	1:J:229:MET:CE	2.46	0.45
1:D:122:ILE:HD13	5:D:600:URM:O20	2.15	0.45
1:H:308:GLU:HB3	1:H:311:HIS:HD2	1.81	0.45
1:I:80:HIS:HB2	1:I:309:PHE:HE2	1.82	0.45
1:D:246:ILE:HB	1:D:250:ILE:HD12	1.99	0.45
1:C:238:MET:HE3	1:F:236:LYS:HB3	1.98	0.45
1:B:182:LYS:HG2	1:B:327:PRO:HG2	1.99	0.45
1:B:90:ASN:HD22	4:B:398:GOL:H2	1.81	0.45
1:D:372:ASN:HB3	2:D:450:FAD:O2	2.17	0.45
1:F:44:LEU:O	1:F:48:LEU:HB2	2.17	0.45
1:I:86:ILE:HG21	1:I:109:HIS:HB2	1.98	0.45
1:A:59:ASP:N	7:A:523:HOH:O	2.48	0.45
1:F:236:LYS:HD3	1:F:236:LYS:HA	1.81	0.45
1:H:84:PRO:HG3	1:H:307:SER:OG	2.16	0.45
1:H:318:HIS:CD2	1:H:319:GLN:HG3	2.52	0.45
1:B:172:TYR:HE2	1:B:177:ARG:HD3	1.81	0.45
1:H:47:ARG:HA	1:H:47:ARG:NE	2.32	0.45
1:J:232:SER:HB3	1:J:235:ILE:HG13	1.97	0.45
1:C:206:ASP:OD1	1:C:208:ARG:HD3	2.16	0.45
1:H:43:VAL:HG21	1:H:377:VAL:HG13	1.99	0.45
1:C:208:ARG:HB3	7:C:401:HOH:O	2.17	0.45
1:E:376:VAL:HG21	2:E:450:FAD:H5'2	1.99	0.45
1:G:30:PHE:O	1:G:252:PHE:HA	2.17	0.45
1:B:138:THR:HG22	1:B:141:GLN:N	2.31	0.44
1:E:269:TYR:OH	1:E:352:LEU:HD21	2.17	0.44
1:J:336:PRO:O	1:J:338:PRO:HD3	2.17	0.44
1:J:305:ARG:NH2	3:J:500:UDP:O3B	2.50	0.44
1:D:158:THR:HA	1:D:191:LEU:O	2.17	0.44
1:I:162:VAL:CG2	1:I:193:ALA:HB1	2.48	0.44
1:A:155:GLN:HB2	1:A:157[A]:ARG:HG3	1.98	0.44
1:B:138:THR:HG23	1:B:139:SER:N	2.30	0.44
1:E:79:ILE:HB	1:E:309:PHE:CD1	2.51	0.44
1:F:242:ASP:HB3	1:F:245:GLU:HG3	1.99	0.44
1:I:206:ASP:OD1	1:I:208:ARG:HD3	2.17	0.44
1:D:298:PRO:HD2	7:D:410:HOH:O	2.16	0.44
1:J:37:ALA:HA	1:J:57:ILE:HD11	1.99	0.44
1:D:369:ARG:HB3	1:D:371:TYR:CE2	2.53	0.44
1:F:289:LEU:CD2	1:F:322:VAL:HG11	2.47	0.44
1:F:297:TYR:HE1	1:F:306:VAL:CG2	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:48:LEU:HD13	1:G:384:PHE:HD1	1.83	0.44
1:I:364:ARG:NH2	1:I:370:TYR:HD2	2.14	0.44
1:E:337:VAL:O	1:E:339:ARG:HG2	2.18	0.44
4:E:400:GOL:O3	4:E:400:GOL:O1	2.30	0.44
1:E:138:THR:HG21	1:H:135:LEU:HD23	1.99	0.44
1:I:272:LEU:HD22	1:I:368:TYR:CZ	2.52	0.44
1:A:58:VAL:HG12	1:A:238:MET:HB3	1.99	0.44
1:B:238:MET:HE1	1:B:241:THR:HG21	1.99	0.44
1:B:318:HIS:HD2	1:B:318:HIS:H	1.56	0.44
1:D:250:ILE:HA	1:D:251:PRO:HD3	1.85	0.44
1:E:289:LEU:N	1:E:308:GLU:OE1	2.48	0.44
1:H:334:TYR:O	1:H:364:ARG:HD3	2.17	0.44
1:G:125:ASN:OD1	1:G:125:ASN:C	2.56	0.44
1:A:364:ARG:HG3	1:A:369:ARG:O	2.18	0.44
1:B:306:VAL:HG13	1:B:324:TYR:CE1	2.52	0.44
1:C:385:ARG:O	1:C:389:GLY:HA2	2.18	0.44
1:D:317:HIS:CE1	1:D:319:GLN:HG3	2.53	0.44
1:H:169:ARG:HB2	1:H:169:ARG:HE	1.63	0.44
1:B:387:LEU:HA	1:B:387:LEU:HD12	1.83	0.43
1:C:112:LEU:HG	1:C:119:LEU:HB3	2.00	0.43
1:E:246:ILE:CD1	1:E:250:ILE:HD12	2.47	0.43
1:E:333:PRO:HG2	1:E:365:LEU:HD13	2.00	0.43
1:G:139:SER:O	1:G:142:VAL:HG12	2.17	0.43
1:I:167:VAL:CG1	1:I:201:THR:HG21	2.47	0.43
1:J:162:VAL:HG21	1:J:193:ALA:HB1	1.97	0.43
1:B:160:GLU:HG2	1:B:164:VAL:HG23	2.00	0.43
1:F:269:TYR:CE2	1:F:352:LEU:CD1	3.01	0.43
1:G:47:ARG:NH1	1:G:100:ARG:HH12	2.16	0.43
1:B:172:TYR:CZ	1:B:177:ARG:HG3	2.53	0.43
1:B:189:SER:HA	1:B:190:GLU:CB	2.30	0.43
1:F:180:THR:HG23	1:F:184:TRP:HD1	1.82	0.43
1:H:105:ARG:NH1	1:H:312:ILE:O	2.51	0.43
1:B:269:TYR:HB2	1:B:349:TYR:CZ	2.54	0.43
1:F:145:PHE:O	1:F:149:VAL:HG22	2.18	0.43
1:F:385:ARG:HE	4:F:400:GOL:C1	2.31	0.43
1:G:124:ILE:HG23	1:G:128:THR:HB	2.00	0.43
1:I:70:ASP:HB2	1:I:79:ILE:O	2.18	0.43
1:B:208:ARG:HD2	1:G:117:GLY:HA2	2.01	0.43
1:C:337:VAL:HG12	1:C:339:ARG:HG3	2.01	0.43
1:C:388:GLN:N	1:C:389:GLY:HA2	2.32	0.43
1:G:187:ASP:CG	1:G:188:PRO:HD2	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:100:ARG:HB3	1:J:100:ARG:HE	1.48	0.43
1:A:77:VAL:O	1:A:79:ILE:HG23	2.19	0.43
1:A:81:PRO:HD2	7:A:537:HOH:O	2.19	0.43
1:B:189:SER:CA	1:B:190:GLU:HB2	2.39	0.43
1:B:191:LEU:CD2	1:B:338:PRO:HD2	2.49	0.43
1:C:218:PRO:HG2	1:C:222:TYR:CD2	2.53	0.43
1:E:336:PRO:C	1:E:338:PRO:HD3	2.38	0.43
1:E:364:ARG:HG2	1:E:365:LEU:HD23	2.00	0.43
1:C:236:LYS:HE3	1:F:245:GLU:OE2	2.18	0.43
1:H:277:LEU:HD23	1:H:327:PRO:HA	2.01	0.43
1:I:31:ASP:O	1:I:253:GLN:HB2	2.19	0.43
1:B:289:LEU:HD12	1:B:289:LEU:HA	1.76	0.43
1:G:125:ASN:OD1	1:G:127:ASP:N	2.52	0.43
1:G:232:SER:HA	1:G:233:PRO:HD3	1.90	0.43
1:J:151:GLU:HB2	1:J:164:VAL:CG1	2.44	0.43
1:J:290:LEU:HD12	1:J:308:GLU:HB2	2.01	0.43
1:D:180:THR:HB	1:D:188:PRO:HG3	2.00	0.43
1:D:242:ASP:HB3	1:D:245:GLU:HG3	1.99	0.43
1:I:383:THR:HG22	1:I:387:LEU:HD22	2.00	0.43
1:B:223:THR:O	1:B:227:GLN:HG3	2.19	0.43
1:F:269:TYR:CZ	1:F:352:LEU:HD11	2.54	0.43
1:G:278:GLU:HB2	1:G:328:ARG:HG3	2.01	0.43
1:A:134:GLY:O	1:G:138:THR:HG22	2.19	0.42
1:C:386:ARG:C	1:C:388:GLN:H	2.23	0.42
1:D:260:PRO:HA	1:D:365:LEU:O	2.19	0.42
1:E:58:VAL:HB	1:E:238:MET:HB3	2.01	0.42
1:E:47:ARG:NE	1:E:47:ARG:HA	2.33	0.42
1:E:59:ASP:OD1	1:E:61:ARG:HG3	2.19	0.42
1:F:261:VAL:HB	1:F:366:ALA:O	2.19	0.42
1:H:29:GLY:CA	1:H:251:PRO:HB2	2.48	0.42
1:J:356:ALA:HB1	1:J:359:VAL:HB	2.00	0.42
1:J:44:LEU:CD1	1:J:362:VAL:HG11	2.49	0.42
1:B:116:ASP:OD2	1:B:174:LYS:HE2	2.18	0.42
1:B:238:MET:CE	1:B:246:ILE:HG21	2.48	0.42
1:C:202:ARG:HB3	1:C:204:ASN:OD1	2.18	0.42
1:D:369:ARG:HB2	1:D:369:ARG:HE	1.66	0.42
1:G:94:VAL:HG13	1:G:377:VAL:HG11	2.01	0.42
1:H:126:LEU:HD23	1:H:142:VAL:HB	2.01	0.42
1:H:262:ASP:HB3	1:H:272:LEU:HB2	2.00	0.42
1:A:250:ILE:HA	1:A:251:PRO:HD3	1.91	0.42
1:B:208:ARG:HD2	1:G:117:GLY:HA3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:ARG:O	1:C:388:GLN:N	2.53	0.42
1:E:277:LEU:HD23	1:E:327:PRO:HA	2.01	0.42
1:F:48:LEU:HA	1:F:48:LEU:HD12	1.95	0.42
1:B:246:ILE:C	1:B:246:ILE:HD12	2.39	0.42
1:B:386:ARG:C	1:B:388:GLN:H	2.23	0.42
1:D:334:TYR:HA	1:D:364:ARG:NH2	2.35	0.42
1:I:125:ASN:OD1	1:I:127:ASP:N	2.51	0.42
1:J:373:MET:HG3	2:J:450:FAD:H2'	2.02	0.42
1:G:359:VAL:HG12	1:G:361:PHE:CE1	2.54	0.42
1:J:364:ARG:NH2	1:J:370:TYR:CD1	2.88	0.42
1:J:47:ARG:HA	1:J:47:ARG:HE	1.85	0.42
1:A:177:ARG:NH1	1:A:181:ARG:HH12	2.18	0.42
1:D:154:GLU:HA	1:D:154:GLU:OE1	2.20	0.42
1:I:44:LEU:CD1	1:I:362:VAL:HG11	2.49	0.42
1:B:277:LEU:HB2	1:B:334:TYR:CE1	2.54	0.42
1:G:189:SER:C	1:G:191:LEU:H	2.23	0.42
1:G:206:ASP:OD2	1:G:208:ARG:NH1	2.52	0.42
1:I:279:PHE:HE2	1:I:325:GLU:HG2	1.84	0.42
1:I:306:VAL:HG13	1:I:324:TYR:CE1	2.54	0.42
1:D:98:LEU:HA	1:D:98:LEU:HD12	1.86	0.42
1:E:108:GLN:HB3	1:E:208:ARG:HG2	2.01	0.42
1:E:171:LEU:HD23	1:E:171:LEU:HA	1.85	0.42
1:E:208:ARG:HD2	1:H:117:GLY:HA3	2.02	0.42
1:G:169:ARG:HE	1:G:169:ARG:HB2	1.71	0.42
1:A:155:GLN:O	1:A:156:VAL:HG23	2.19	0.42
1:H:341:GLU:O	1:H:344:GLU:HG2	2.20	0.42
1:H:90:ASN:OD1	1:H:212:ASP:HA	2.20	0.42
1:J:198:ARG:O	1:J:200:PRO:HD3	2.20	0.41
1:A:179:TYR:CD2	3:A:500:UDP:H2'	2.55	0.41
1:E:58:VAL:HA	1:E:238:MET:O	2.20	0.41
1:G:250:ILE:HA	1:G:251:PRO:HD3	1.82	0.41
1:G:290:LEU:HD12	1:G:308:GLU:HB2	2.01	0.41
1:I:362:VAL:HG23	1:I:379:GLN:OE1	2.21	0.41
1:I:79:ILE:O	1:I:80:HIS:HD2	2.02	0.41
1:A:169:ARG:HG2	1:A:173:ASN:HD21	1.86	0.41
1:B:246:ILE:HD13	1:B:250:ILE:HD12	2.01	0.41
1:C:32:TYR:HA	1:C:254:HIS:O	2.21	0.41
1:F:250:ILE:HA	1:F:251:PRO:HD3	1.84	0.41
1:F:306:VAL:HG13	1:F:324:TYR:CD1	2.55	0.41
1:G:119:LEU:HD23	1:G:119:LEU:HA	1.84	0.41
1:G:102:THR:HB	1:G:225:MET:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:250:ILE:O	1:D:252:PHE:CD2	2.73	0.41
1:D:320:THR:HG23	1:D:320:THR:O	2.19	0.41
1:E:117:GLY:HA3	1:I:208:ARG:HD2	2.02	0.41
1:F:185:GLY:O	1:F:186:LEU:HD12	2.20	0.41
1:A:155:GLN:HB2	1:A:157[A]:ARG:CG	2.51	0.41
1:B:126:LEU:HD23	1:B:142:VAL:HG21	2.00	0.41
1:B:338:PRO:O	1:B:339:ARG:HG3	2.20	0.41
1:E:242:ASP:HB3	1:E:245:GLU:HG3	2.02	0.41
1:F:114:SER:HA	1:F:118:GLN:O	2.20	0.41
1:I:373:MET:HB2	1:I:373:MET:HE3	1.92	0.41
1:J:32:TYR:HA	1:J:254:HIS:O	2.21	0.41
1:A:154:GLU:CG	1:A:155:GLN:H	2.16	0.41
1:D:182:LYS:HG2	1:D:304:THR:CG2	2.50	0.41
1:E:364:ARG:NH2	1:E:370:TYR:HD1	2.18	0.41
1:E:377:VAL:O	1:E:381:LEU:HG	2.20	0.41
1:E:34:ILE:HG12	1:E:256:ILE:HB	2.01	0.41
1:E:98:LEU:HD12	1:E:98:LEU:HA	1.94	0.41
1:F:124:ILE:HB	1:F:201:THR:HG23	2.03	0.41
1:H:171:LEU:HA	1:H:171:LEU:HD23	1.90	0.41
1:B:389:GLY:O	1:B:390:GLN:C	2.58	0.41
1:E:348:LYS:O	1:E:351:ALA:HB3	2.21	0.41
1:A:162:VAL:O	1:A:166:LYS:HE3	2.21	0.41
1:E:371:TYR:HE2	1:E:379:GLN:HE22	1.68	0.41
1:F:154:GLU:OE1	1:F:154:GLU:HA	2.21	0.41
1:F:37:ALA:HA	1:F:57:ILE:HD11	2.03	0.41
1:G:308:GLU:HB3	1:G:311:HIS:HD2	1.86	0.41
1:I:159:SER:HB3	1:I:196:THR:HG23	2.03	0.41
1:J:273:PRO:HG2	1:J:342:ASN:OD1	2.21	0.41
1:E:120:LEU:HA	1:E:120:LEU:HD12	1.97	0.41
1:A:97:TYR:O	1:A:100:ARG:HG3	2.21	0.41
1:A:159:SER:HB2	1:A:188:PRO:O	2.21	0.41
1:B:159:SER:OG	1:B:192:ASP:O	2.25	0.41
1:E:169:ARG:HG3	1:E:173:ASN:HD21	1.85	0.41
1:E:204:ASN:C	1:E:204:ASN:OD1	2.59	0.41
1:G:364:ARG:HD3	2:G:450:FAD:H3'	2.03	0.41
1:I:275:ARG:HB3	1:I:335:TYR:HB2	2.02	0.41
1:J:300:ASP:O	1:J:301:TYR:HB2	2.20	0.41
1:A:169:ARG:HG2	1:A:173:ASN:ND2	2.35	0.40
1:B:277:LEU:HB2	1:B:334:TYR:CD1	2.57	0.40
1:C:250:ILE:HA	1:C:251:PRO:HD3	1.82	0.40
1:C:30:PHE:CE1	1:C:56:LEU:HD22	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:289:LEU:HD11	6:I:401:XYL:H4	2.04	0.40
1:J:162:VAL:HG23	1:J:193:ALA:HB1	1.99	0.40
1:A:102:THR:HB	1:A:225:MET:HG3	2.03	0.40
1:A:318:HIS:H	1:A:318:HIS:CD2	2.39	0.40
1:A:345:LEU:HA	1:A:345:LEU:HD23	1.80	0.40
1:C:341:GLU:HG3	1:C:341:GLU:H	1.41	0.40
1:F:308:GLU:HB3	1:F:311:HIS:HD2	1.86	0.40
1:I:373:MET:O	1:I:377:VAL:HG23	2.21	0.40
1:A:104:TRP:HB3	1:A:216:ALA:HB1	2.04	0.40
1:G:172:TYR:OH	1:G:188:PRO:HG2	2.21	0.40
1:G:77:VAL:HG11	1:G:321:SER:HB2	2.03	0.40
1:I:67:ASN:HD21	2:I:450:FAD:HM81	1.85	0.40
1:J:265:PHE:HZ	1:J:353:ALA:HA	1.86	0.40
1:A:210:PHE:HB3	1:A:212:ASP:OD2	2.21	0.40
1:D:333:PRO:O	1:D:364:ARG:NH2	2.47	0.40
1:H:137:LEU:HD12	1:H:142:VAL:HG23	2.03	0.40
1:J:159:SER:HB3	1:J:196:THR:CG2	2.52	0.40
1:A:229:MET:HB2	1:A:229:MET:HE2	1.92	0.40
1:A:306:VAL:HG22	1:A:324:TYR:CD1	2.57	0.40
1:B:160:GLU:HB2	1:B:189:SER:OG	2.21	0.40
1:C:73:ASP:HB2	7:C:438:HOH:O	2.22	0.40
1:F:371:TYR:HB3	1:F:376:VAL:HG23	2.03	0.40
1:J:114:SER:HA	1:J:118:GLN:O	2.21	0.40
1:J:272:LEU:CD2	1:J:368:TYR:CZ	3.05	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	364/397 (92%)	349 (96%)	12 (3%)	3 (1%)	22 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	361/397 (91%)	331 (92%)	24 (7%)	6 (2%)	11	16
1	C	361/397 (91%)	341 (94%)	17 (5%)	3 (1%)	22	34
1	D	357/397 (90%)	333 (93%)	22 (6%)	2 (1%)	28	43
1	E	359/397 (90%)	329 (92%)	27 (8%)	3 (1%)	22	34
1	F	363/397 (91%)	351 (97%)	12 (3%)	0	100	100
1	G	361/397 (91%)	345 (96%)	15 (4%)	1 (0%)	44	62
1	H	362/397 (91%)	342 (94%)	20 (6%)	0	100	100
1	I	362/397 (91%)	342 (94%)	20 (6%)	0	100	100
1	J	361/397 (91%)	340 (94%)	17 (5%)	4 (1%)	17	26
All	All	3611/3970 (91%)	3403 (94%)	186 (5%)	22 (1%)	28	43

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	GLU
1	B	150	ALA
1	B	188	PRO
1	C	357	GLN
1	B	186	LEU
1	B	200	PRO
1	B	167	VAL
1	C	154	GLU
1	E	355	ALA
1	J	357	GLN
1	E	156	VAL
1	J	154	GLU
1	J	268	CYS
1	C	387	LEU
1	D	154	GLU
1	D	387	LEU
1	G	340	PRO
1	J	266	ASP
1	A	195	VAL
1	A	164	VAL
1	B	187	ASP
1	E	338	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	318/346 (92%)	295 (93%)	23 (7%)	17	27
1	B	315/346 (91%)	300 (95%)	15 (5%)	30	46
1	C	315/346 (91%)	293 (93%)	22 (7%)	18	28
1	D	313/346 (90%)	297 (95%)	16 (5%)	28	43
1	E	313/346 (90%)	293 (94%)	20 (6%)	20	33
1	F	317/346 (92%)	297 (94%)	20 (6%)	21	34
1	G	315/346 (91%)	302 (96%)	13 (4%)	35	54
1	H	316/346 (91%)	294 (93%)	22 (7%)	18	28
1	I	316/346 (91%)	295 (93%)	21 (7%)	19	31
1	J	315/346 (91%)	296 (94%)	19 (6%)	22	36
All	All	3153/3460 (91%)	2962 (94%)	191 (6%)	22	35

All (191) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	44	LEU
1	A	48	LEU
1	A	98	LEU
1	A	112	LEU
1	A	120	LEU
1	A	156	VAL
1	A	157[A]	ARG
1	A	157[B]	ARG
1	A	159	SER
1	A	164	VAL
1	A	208	ARG
1	A	212	ASP
1	A	261	VAL
1	A	272	LEU
1	A	282	GLU

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Mol	Chain	Res	Type
1	A	339	ARG
1	A	341	GLU
1	A	344	GLU
1	A	345	LEU
1	A	362	VAL
1	A	370	TYR
1	A	387	LEU
1	B	98	LEU
1	B	112	LEU
1	B	120	LEU
1	B	126	LEU
1	B	138	THR
1	B	169	ARG
1	B	172	TYR
1	B	187	ASP
1	B	261	VAL
1	B	292	THR
1	B	306	VAL
1	B	318	HIS
1	B	341	GLU
1	B	345	LEU
1	B	387	LEU
1	C	34	ILE
1	C	48	LEU
1	C	98	LEU
1	C	112	LEU
1	C	120	LEU
1	C	126	LEU
1	C	148	SER
1	C	154	GLU
1	C	159	SER
1	C	164	VAL
1	C	182	LYS
1	C	183	GLN
1	C	186	LEU
1	C	261	VAL
1	C	286	THR
1	C	330	GLU
1	C	341	GLU
1	C	345	LEU
1	C	347	LYS
1	C	369	ARG

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Mol	Chain	Res	Type
1	C	388	GLN
1	C	390	GLN
1	D	60	ARG
1	D	61	ARG
1	D	98	LEU
1	D	112	LEU
1	D	120	LEU
1	D	126	LEU
1	D	142	VAL
1	D	154	GLU
1	D	165	SER
1	D	172	TYR
1	D	212	ASP
1	D	261	VAL
1	D	300	ASP
1	D	319	GLN
1	D	362	VAL
1	D	387	LEU
1	E	31	ASP
1	E	48	LEU
1	E	60	ARG
1	E	79	ILE
1	E	98	LEU
1	E	112	LEU
1	E	120	LEU
1	E	126	LEU
1	E	164	VAL
1	E	192	ASP
1	E	212	ASP
1	E	227	GLN
1	E	254	HIS
1	E	258	THR
1	E	261	VAL
1	E	330	GLU
1	E	341	GLU
1	E	362	VAL
1	E	370	TYR
1	E	387	LEU
1	F	44	LEU
1	F	48	LEU
1	F	58	VAL
1	F	98	LEU

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Mol	Chain	Res	Type
1	F	112	LEU
1	F	120	LEU
1	F	126	LEU
1	F	149	VAL
1	F	159	SER
1	F	164	VAL
1	F	182	LYS
1	F	192	ASP
1	F	272	LEU
1	F	306	VAL
1	F	330	GLU
1	F	345	LEU
1	F	362	VAL
1	F	369	ARG
1	F	370	TYR
1	F	387	LEU
1	G	48	LEU
1	G	98	LEU
1	G	112	LEU
1	G	120	LEU
1	G	126	LEU
1	G	148	SER
1	G	155	GLN
1	G	157	ARG
1	G	159	SER
1	G	282	GLU
1	G	330	GLU
1	G	362	VAL
1	G	370	TYR
1	H	48	LEU
1	H	51	SER
1	H	60	ARG
1	H	98	LEU
1	H	112	LEU
1	H	120	LEU
1	H	126	LEU
1	H	139	SER
1	H	155	GLN
1	H	169	ARG
1	H	232	SER
1	H	253	GLN
1	H	261	VAL

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Mol	Chain	Res	Type
1	H	272	LEU
1	H	305	ARG
1	H	306	VAL
1	H	330	GLU
1	H	339	ARG
1	H	340	PRO
1	H	345	LEU
1	H	370	TYR
1	H	387	LEU
1	I	44	LEU
1	I	48	LEU
1	I	54	ARG
1	I	64	ILE
1	I	98	LEU
1	I	112	LEU
1	I	120	LEU
1	I	122	ILE
1	I	126	LEU
1	I	153	VAL
1	I	164	VAL
1	I	186	LEU
1	I	261	VAL
1	I	272	LEU
1	I	306	VAL
1	I	339	ARG
1	I	344	GLU
1	I	345	LEU
1	I	364	ARG
1	I	370	TYR
1	I	387	LEU
1	J	48	LEU
1	J	60	ARG
1	J	98	LEU
1	J	112	LEU
1	J	120	LEU
1	J	126	LEU
1	J	136	ASN
1	J	186	LEU
1	J	212	ASP
1	J	227	GLN
1	J	245	GLU
1	J	272	LEU

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Mol	Chain	Res	Type
1	J	282	GLU
1	J	305	ARG
1	J	316	ARG
1	J	330	GLU
1	J	341	GLU
1	J	370	TYR
1	J	387	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	HIS
1	B	318	HIS
1	C	388	GLN
1	D	67	ASN
1	D	183	GLN
1	D	220	HIS
1	D	311	HIS
1	D	319	GLN
1	E	90	ASN
1	E	173	ASN
1	F	390	GLN
1	G	253	GLN
1	G	281	HIS
1	H	253	GLN
1	H	311	HIS
1	I	67	ASN
1	I	253	GLN
1	I	311	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

47 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	GOL	A	398	-	5,5,5	0.29	0	5,5,5	0.51	0
4	GOL	A	399	-	5,5,5	0.46	0	5,5,5	0.31	0
4	GOL	A	400	-	5,5,5	0.33	0	5,5,5	0.11	0
2	FAD	A	450	-	51,58,58	1.26	5 (9%)	54,89,89	1.95	6 (11%)
3	UDP	A	500	-	21,26,26	1.03	1 (4%)	22,40,40	1.44	1 (4%)
4	GOL	B	398	-	5,5,5	0.41	0	5,5,5	0.33	0
2	FAD	B	450	-	51,58,58	1.29	6 (11%)	54,89,89	1.98	7 (12%)
3	UDP	B	500	-	21,26,26	1.10	1 (4%)	22,40,40	1.79	2 (9%)
4	GOL	C	398	-	5,5,5	0.31	0	5,5,5	0.27	0
4	GOL	C	399	-	5,5,5	0.34	0	5,5,5	0.36	0
2	FAD	C	450	-	51,58,58	1.31	6 (11%)	54,89,89	1.89	5 (9%)
3	UDP	C	500	-	21,26,26	0.96	1 (4%)	22,40,40	1.57	1 (4%)
4	GOL	D	398	-	5,5,5	0.27	0	5,5,5	0.59	0
4	GOL	D	399	-	5,5,5	0.42	0	5,5,5	0.53	0
2	FAD	D	450	-	51,58,58	1.25	5 (9%)	54,89,89	1.97	6 (11%)
5	URM	D	600	-	32,38,38	2.64	5 (15%)	37,58,58	1.43	5 (13%)
4	GOL	E	398	-	5,5,5	0.35	0	5,5,5	0.49	0
4	GOL	E	399	-	5,5,5	0.34	0	5,5,5	0.20	0
4	GOL	E	400	-	5,5,5	0.24	0	5,5,5	0.46	0
4	GOL	E	401	-	5,5,5	0.33	0	5,5,5	0.35	0
2	FAD	E	450	-	51,58,58	1.26	7 (13%)	54,89,89	1.94	6 (11%)
3	UDP	E	500	-	18,22,26	1.06	1 (5%)	22,33,40	1.76	2 (9%)
4	GOL	F	398	-	5,5,5	0.25	0	5,5,5	0.67	0
6	XYL	F	399	-	9,9,9	1.67	2 (22%)	11,11,11	1.67	3 (27%)
4	GOL	F	400	-	5,5,5	0.38	0	5,5,5	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FAD	F	450	-	51,58,58	1.35	6 (11%)	54,89,89	2.03	7 (12%)
3	UDP	F	500	-	21,26,26	1.14	1 (4%)	22,40,40	1.69	1 (4%)
4	GOL	G	398	-	5,5,5	0.38	0	5,5,5	0.31	0
4	GOL	G	399	-	5,5,5	0.34	0	5,5,5	0.52	0
4	GOL	G	400	-	5,5,5	0.35	0	5,5,5	0.37	0
2	FAD	G	450	-	51,58,58	1.29	7 (13%)	54,89,89	1.96	6 (11%)
3	UDP	G	500	-	21,26,26	1.07	1 (4%)	22,40,40	1.48	1 (4%)
4	GOL	H	398	-	5,5,5	0.31	0	5,5,5	0.38	0
4	GOL	H	399	-	5,5,5	0.42	0	5,5,5	0.29	0
2	FAD	H	450	-	51,58,58	1.31	6 (11%)	54,89,89	1.78	6 (11%)
3	UDP	H	500	-	21,26,26	1.07	1 (4%)	22,40,40	1.30	1 (4%)
4	GOL	I	398	-	5,5,5	0.34	0	5,5,5	0.75	0
4	GOL	I	399	-	5,5,5	0.38	0	5,5,5	0.49	0
4	GOL	I	400	-	5,5,5	0.32	0	5,5,5	0.30	0
6	XYL	I	401	-	9,9,9	1.22	2 (22%)	11,11,11	2.45	4 (36%)
4	GOL	I	402	-	5,5,5	0.35	0	5,5,5	0.45	0
2	FAD	I	450	-	51,58,58	1.24	6 (11%)	54,89,89	1.79	5 (9%)
3	UDP	I	500	-	18,22,26	1.17	1 (5%)	22,33,40	1.55	1 (4%)
4	GOL	J	399	-	5,5,5	0.48	0	5,5,5	0.38	0
4	GOL	J	400	-	5,5,5	0.39	0	5,5,5	0.45	0
2	FAD	J	450	-	51,58,58	1.29	6 (11%)	54,89,89	1.94	5 (9%)
3	UDP	J	500	-	21,26,26	1.10	1 (4%)	22,40,40	1.32	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	398	-	-	0/4/4/4	0/0/0/0
4	GOL	A	399	-	-	0/4/4/4	0/0/0/0
4	GOL	A	400	-	-	0/4/4/4	0/0/0/0
2	FAD	A	450	-	-	0/28/50/50	0/6/6/6
3	UDP	A	500	-	-	0/12/32/32	0/2/2/2
4	GOL	B	398	-	-	0/4/4/4	0/0/0/0
2	FAD	B	450	-	-	0/28/50/50	0/6/6/6
3	UDP	B	500	-	-	0/12/32/32	0/2/2/2
4	GOL	C	398	-	-	0/4/4/4	0/0/0/0
4	GOL	C	399	-	-	0/4/4/4	0/0/0/0
2	FAD	C	450	-	-	0/28/50/50	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	UDP	C	500	-	-	0/12/32/32	0/2/2/2
4	GOL	D	398	-	-	0/4/4/4	0/0/0/0
4	GOL	D	399	-	-	0/4/4/4	0/0/0/0
2	FAD	D	450	-	-	0/28/50/50	0/6/6/6
5	URM	D	600	-	-	0/16/59/59	0/3/3/3
4	GOL	E	398	-	-	0/4/4/4	0/0/0/0
4	GOL	E	399	-	-	0/4/4/4	0/0/0/0
4	GOL	E	400	-	-	0/4/4/4	0/0/0/0
4	GOL	E	401	-	-	0/4/4/4	0/0/0/0
2	FAD	E	450	-	-	0/28/50/50	0/6/6/6
3	UDP	E	500	-	-	0/6/26/32	0/2/2/2
4	GOL	F	398	-	-	0/4/4/4	0/0/0/0
6	XYL	F	399	-	-	0/12/12/12	0/0/0/0
4	GOL	F	400	-	-	0/4/4/4	0/0/0/0
2	FAD	F	450	-	-	0/28/50/50	0/6/6/6
3	UDP	F	500	-	-	0/12/32/32	0/2/2/2
4	GOL	G	398	-	-	0/4/4/4	0/0/0/0
4	GOL	G	399	-	-	0/4/4/4	0/0/0/0
4	GOL	G	400	-	-	0/4/4/4	0/0/0/0
2	FAD	G	450	-	-	0/28/50/50	0/6/6/6
3	UDP	G	500	-	-	0/12/32/32	0/2/2/2
4	GOL	H	398	-	-	0/4/4/4	0/0/0/0
4	GOL	H	399	-	-	0/4/4/4	0/0/0/0
2	FAD	H	450	-	-	0/28/50/50	0/6/6/6
3	UDP	H	500	-	-	0/12/32/32	0/2/2/2
4	GOL	I	398	-	-	0/4/4/4	0/0/0/0
4	GOL	I	399	-	-	0/4/4/4	0/0/0/0
4	GOL	I	400	-	-	0/4/4/4	0/0/0/0
6	XYL	I	401	-	-	0/12/12/12	0/0/0/0
4	GOL	I	402	-	-	0/4/4/4	0/0/0/0
2	FAD	I	450	-	-	0/28/50/50	0/6/6/6
3	UDP	I	500	-	-	0/6/26/32	0/2/2/2
4	GOL	J	399	-	-	0/4/4/4	0/0/0/0
4	GOL	J	400	-	-	0/4/4/4	0/0/0/0
2	FAD	J	450	-	-	0/28/50/50	0/6/6/6
3	UDP	J	500	-	-	0/12/32/32	0/2/2/2

All (78) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	600	URM	P22-C45	-12.07	1.61	1.80
5	D	600	URM	C19-N15	-5.55	1.27	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	399	XYL	O2-C2	-3.55	1.35	1.43
6	F	399	XYL	O4-C4	-2.57	1.37	1.43
5	D	600	URM	P22-O23	-2.56	1.50	1.56
6	I	401	XYL	O2-C2	-2.41	1.38	1.43
6	I	401	XYL	O4-C4	-2.01	1.38	1.43
2	E	450	FAD	C5X-N5	2.00	1.38	1.35
2	G	450	FAD	C1'-N10	2.00	1.50	1.48
2	E	450	FAD	C1'-N10	2.01	1.50	1.48
5	D	600	URM	P22-O12	2.01	1.60	1.58
2	I	450	FAD	C5X-N5	2.02	1.38	1.35
2	G	450	FAD	C5X-N5	2.16	1.38	1.35
2	H	450	FAD	C5X-N5	2.16	1.38	1.35
2	B	450	FAD	C5X-N5	2.28	1.38	1.35
2	C	450	FAD	C5X-N5	2.29	1.38	1.35
2	J	450	FAD	C2A-N1A	2.34	1.38	1.33
2	D	450	FAD	C2A-N1A	2.42	1.38	1.33
2	F	450	FAD	C5X-N5	2.44	1.39	1.35
2	B	450	FAD	C2A-N1A	2.51	1.38	1.33
2	I	450	FAD	C2A-N1A	2.51	1.38	1.33
2	J	450	FAD	C1'-N10	2.51	1.51	1.48
3	A	500	UDP	C4-N3	2.56	1.37	1.33
2	C	450	FAD	C2A-N1A	2.57	1.38	1.33
2	F	450	FAD	C2A-N1A	2.58	1.38	1.33
2	A	450	FAD	C4-N3	2.59	1.37	1.33
2	H	450	FAD	C2A-N1A	2.63	1.38	1.33
3	C	500	UDP	C4-N3	2.68	1.37	1.33
2	D	450	FAD	C10-N1	2.69	1.37	1.33
2	A	450	FAD	C2A-N1A	2.71	1.39	1.33
2	E	450	FAD	C2A-N1A	2.72	1.39	1.33
3	E	500	UDP	C4-N3	2.73	1.38	1.33
5	D	600	URM	O6-C1	2.74	1.45	1.41
2	G	450	FAD	C2A-N1A	2.76	1.39	1.33
2	I	450	FAD	C4-N3	2.79	1.38	1.33
2	J	450	FAD	C4X-N5	2.89	1.37	1.33
2	I	450	FAD	C4X-N5	2.90	1.37	1.33
3	F	500	UDP	C4-N3	2.92	1.38	1.33
3	H	500	UDP	C4-N3	3.00	1.38	1.33
3	J	500	UDP	C4-N3	3.01	1.38	1.33
2	D	450	FAD	C4X-N5	3.03	1.37	1.33
2	F	450	FAD	C4-N3	3.07	1.38	1.33
2	B	450	FAD	C10-N1	3.07	1.37	1.33
2	E	450	FAD	C4-N3	3.10	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	450	FAD	C4-N3	3.11	1.38	1.33
3	G	500	UDP	C4-N3	3.12	1.38	1.33
2	J	450	FAD	C4-N3	3.14	1.38	1.33
2	E	450	FAD	C10-N1	3.15	1.37	1.33
2	G	450	FAD	C10-N1	3.21	1.37	1.33
2	C	450	FAD	C4-N3	3.23	1.38	1.33
2	H	450	FAD	C4X-N5	3.24	1.38	1.33
3	I	500	UDP	C4-N3	3.26	1.38	1.33
2	D	450	FAD	C4-N3	3.26	1.38	1.33
3	B	500	UDP	C4-N3	3.27	1.39	1.33
2	B	450	FAD	C4-N3	3.33	1.39	1.33
2	B	450	FAD	C4X-N5	3.34	1.38	1.33
2	H	450	FAD	C4-N3	3.36	1.39	1.33
2	A	450	FAD	C4X-N5	3.38	1.38	1.33
2	E	450	FAD	C4X-N5	3.51	1.38	1.33
2	G	450	FAD	C4X-N5	3.53	1.38	1.33
2	H	450	FAD	C10-N1	3.53	1.38	1.33
2	I	450	FAD	C10-N1	3.55	1.38	1.33
2	C	450	FAD	C10-N1	3.55	1.38	1.33
2	F	450	FAD	C2A-N3A	3.61	1.38	1.32
2	B	450	FAD	C2A-N3A	3.64	1.38	1.32
2	A	450	FAD	C10-N1	3.66	1.38	1.33
2	J	450	FAD	C10-N1	3.67	1.38	1.33
2	D	450	FAD	C2A-N3A	3.77	1.38	1.32
2	F	450	FAD	C10-N1	3.78	1.38	1.33
2	H	450	FAD	C2A-N3A	3.82	1.38	1.32
2	C	450	FAD	C4X-N5	3.86	1.38	1.33
2	E	450	FAD	C2A-N3A	3.92	1.38	1.32
2	J	450	FAD	C2A-N3A	3.97	1.38	1.32
2	F	450	FAD	C4X-N5	3.98	1.39	1.33
2	A	450	FAD	C2A-N3A	4.10	1.39	1.32
2	G	450	FAD	C2A-N3A	4.11	1.39	1.32
2	I	450	FAD	C2A-N3A	4.20	1.39	1.32
2	C	450	FAD	C2A-N3A	4.23	1.39	1.32

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	450	FAD	N3A-C2A-N1A	-11.20	119.10	128.86
2	F	450	FAD	N3A-C2A-N1A	-10.64	119.59	128.86
2	D	450	FAD	N3A-C2A-N1A	-10.39	119.81	128.86
2	G	450	FAD	N3A-C2A-N1A	-10.37	119.83	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	450	FAD	N3A-C2A-N1A	-10.24	119.94	128.86
2	A	450	FAD	N3A-C2A-N1A	-9.80	120.32	128.86
2	I	450	FAD	N3A-C2A-N1A	-9.63	120.47	128.86
2	E	450	FAD	N3A-C2A-N1A	-9.28	120.78	128.86
2	H	450	FAD	N3A-C2A-N1A	-9.11	120.92	128.86
2	C	450	FAD	N3A-C2A-N1A	-9.01	121.01	128.86
5	D	600	URM	C18-N13-C19	-4.07	114.69	121.28
2	E	450	FAD	C4X-C4-N3	-3.82	118.05	123.48
2	G	450	FAD	C4X-C4-N3	-3.22	118.90	123.48
2	D	450	FAD	C4X-C4-N3	-3.18	118.96	123.48
2	B	450	FAD	C4X-C4-N3	-3.11	119.06	123.48
2	I	450	FAD	C4X-C4-N3	-3.09	119.09	123.48
2	A	450	FAD	C4X-C4-N3	-2.99	119.22	123.48
2	F	450	FAD	C4X-C4-N3	-2.96	119.26	123.48
2	H	450	FAD	C4X-C4-N3	-2.87	119.40	123.48
2	J	450	FAD	C4X-C4-N3	-2.81	119.48	123.48
2	C	450	FAD	C4X-C4-N3	-2.59	119.80	123.48
2	A	450	FAD	O4'-C4'-C5'	-2.08	105.37	110.00
5	D	600	URM	P9-O12-P22	-2.06	125.75	132.39
6	F	399	XYL	O2-C2-C3	-2.04	104.03	109.09
2	B	450	FAD	C4A-C5A-N7A	-2.03	107.45	109.41
2	F	450	FAD	C5A-C6A-N6A	-2.01	116.37	120.47
5	D	600	URM	C17-C20-N15	-2.00	118.34	123.12
2	E	450	FAD	C4-C4X-N5	2.03	120.91	118.68
2	D	450	FAD	C4X-N5-C5X	2.05	118.93	116.76
3	B	500	UDP	O4'-C1'-N1	2.09	112.26	108.08
2	F	450	FAD	C5X-C9A-N10	2.23	119.31	117.66
2	D	450	FAD	C5X-C9A-N10	2.31	119.37	117.66
2	H	450	FAD	C5X-C9A-N10	2.36	119.41	117.66
3	E	500	UDP	O4'-C1'-N1	2.38	112.84	108.08
2	B	450	FAD	C1'-N10-C9A	2.39	120.54	118.35
2	B	450	FAD	C4-C4X-N5	2.46	121.38	118.68
6	F	399	XYL	O5-C5-C4	2.47	116.56	111.11
2	F	450	FAD	C1'-N10-C9A	2.56	120.69	118.35
2	G	450	FAD	C1'-N10-C9A	2.69	120.81	118.35
2	I	450	FAD	C4X-N5-C5X	2.69	119.61	116.76
2	C	450	FAD	C1'-N10-C10	2.71	121.28	118.50
2	H	450	FAD	C4X-N5-C5X	2.75	119.67	116.76
6	I	401	XYL	O3-C3-C4	2.75	115.64	108.82
2	I	450	FAD	C1'-N10-C9A	2.84	120.95	118.35
6	I	401	XYL	O3-C3-C2	2.94	116.10	108.82
5	D	600	URM	O6-C4-C5	2.99	119.48	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	450	FAD	C4X-N5-C5X	2.99	119.92	116.76
2	G	450	FAD	C5X-C9A-N10	3.07	119.93	117.66
2	A	450	FAD	C1'-N10-C9A	3.11	121.19	118.35
5	D	600	URM	O6-C1-N13	3.13	114.35	108.08
2	F	450	FAD	C4X-N5-C5X	3.24	120.18	116.76
2	J	450	FAD	C4X-N5-C5X	3.37	120.32	116.76
2	H	450	FAD	C1'-N10-C9A	3.50	121.55	118.35
6	F	399	XYL	O1-C1-C2	3.50	118.83	111.11
2	E	450	FAD	C4X-N5-C5X	3.57	120.53	116.76
6	I	401	XYL	O5-C5-C4	3.57	118.99	111.11
2	B	450	FAD	C4X-N5-C5X	3.57	120.54	116.76
2	A	450	FAD	C4X-N5-C5X	3.59	120.55	116.76
2	E	450	FAD	C1'-N10-C9A	3.74	121.78	118.35
2	C	450	FAD	C5X-C9A-N10	4.27	120.83	117.66
2	D	450	FAD	C1'-N10-C9A	4.32	122.30	118.35
2	J	450	FAD	C4-N3-C2	4.69	119.27	115.16
2	J	450	FAD	C1'-N10-C9A	4.76	122.71	118.35
6	I	401	XYL	O1-C1-C2	5.14	122.46	111.11
2	I	450	FAD	C4-N3-C2	5.27	119.77	115.16
2	B	450	FAD	C4-N3-C2	5.37	119.85	115.16
3	J	500	UDP	C4-N3-C2	5.46	118.82	114.13
3	H	500	UDP	C4-N3-C2	5.51	118.86	114.13
2	H	450	FAD	C4-N3-C2	5.71	120.16	115.16
2	G	450	FAD	C4-N3-C2	5.76	120.20	115.16
3	A	500	UDP	C4-N3-C2	5.85	119.16	114.13
2	D	450	FAD	C4-N3-C2	5.90	120.32	115.16
2	A	450	FAD	C4-N3-C2	6.18	120.56	115.16
2	C	450	FAD	C4-N3-C2	6.19	120.57	115.16
3	G	500	UDP	C4-N3-C2	6.22	119.47	114.13
3	I	500	UDP	C4-N3-C2	6.28	119.52	114.13
3	C	500	UDP	C4-N3-C2	6.39	119.62	114.13
3	F	500	UDP	C4-N3-C2	6.71	119.90	114.13
2	F	450	FAD	C4-N3-C2	6.77	121.08	115.16
2	E	450	FAD	C4-N3-C2	6.78	121.09	115.16
3	E	500	UDP	C4-N3-C2	6.92	120.08	114.13
3	B	500	UDP	C4-N3-C2	7.39	120.48	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

25 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	398	GOL	1	0
2	A	450	FAD	2	0
3	A	500	UDP	1	0
4	B	398	GOL	2	0
2	B	450	FAD	1	0
3	B	500	UDP	4	0
4	C	398	GOL	2	0
2	C	450	FAD	1	0
4	D	399	GOL	1	0
2	D	450	FAD	5	0
5	D	600	URM	1	0
4	E	398	GOL	1	0
4	E	400	GOL	1	0
2	E	450	FAD	3	0
4	F	398	GOL	1	0
4	F	400	GOL	1	0
2	G	450	FAD	1	0
3	G	500	UDP	1	0
4	H	398	GOL	2	0
4	I	398	GOL	3	0
6	I	401	XYL	1	0
4	I	402	GOL	2	0
2	I	450	FAD	3	0
2	J	450	FAD	1	0
3	J	500	UDP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	365/397 (91%)	-0.13	6 (1%) 72 72	32, 43, 60, 93	1 (0%)
1	B	363/397 (91%)	0.43	45 (12%) 4 3	35, 47, 94, 152	1 (0%)
1	C	363/397 (91%)	0.02	11 (3%) 51 49	36, 49, 71, 104	1 (0%)
1	D	359/397 (90%)	0.56	45 (12%) 4 3	38, 55, 80, 120	2 (0%)
1	E	361/397 (90%)	0.40	33 (9%) 10 8	38, 59, 91, 122	2 (0%)
1	F	364/397 (91%)	0.08	12 (3%) 47 45	37, 49, 68, 95	2 (0%)
1	G	363/397 (91%)	-0.05	6 (1%) 70 70	34, 53, 78, 126	2 (0%)
1	H	364/397 (91%)	0.00	9 (2%) 58 56	35, 48, 69, 115	1 (0%)
1	I	364/397 (91%)	-0.14	6 (1%) 72 72	33, 46, 66, 113	1 (0%)
1	J	363/397 (91%)	0.31	34 (9%) 9 7	36, 53, 81, 109	3 (0%)
All	All	3629/3970 (91%)	0.15	207 (5%) 24 22	32, 49, 81, 152	16 (0%)

All (207) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	VAL	7.4
1	B	153	VAL	7.3
1	B	186	LEU	6.1
1	E	154	GLU	5.7
1	E	153	VAL	5.7
1	B	162	VAL	5.4
1	D	361	PHE	5.2
1	E	269	TYR	5.1
1	E	157	ARG	5.0
1	D	163	VAL	4.9
1	B	156	VAL	4.9
1	B	157	ARG	4.8
1	J	269	TYR	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	196	THR	4.7
1	D	369	ARG	4.7
1	E	156	VAL	4.7
1	B	159	SER	4.6
1	J	387	LEU	4.6
1	B	390	GLN	4.4
1	E	271	LYS	4.4
1	B	155	GLN	4.3
1	E	389	GLY	4.2
1	H	389	GLY	4.1
1	B	161	ASP	4.1
1	D	153	VAL	4.0
1	H	27	SER	4.0
1	D	249	PHE	4.0
1	B	189	SER	3.9
1	F	318	HIS	3.9
1	E	163	VAL	3.9
1	E	152	LYS	3.9
1	C	153	VAL	3.9
1	J	270	GLY	3.8
1	D	265	PHE	3.8
1	D	156	VAL	3.8
1	D	162	VAL	3.8
1	J	386	ARG	3.8
1	E	155	GLN	3.8
1	F	154	GLU	3.7
1	J	344	GLU	3.7
1	D	254	HIS	3.6
1	B	195	VAL	3.6
1	B	172	TYR	3.6
1	F	253	GLN	3.6
1	B	167	VAL	3.6
1	D	357	GLN	3.6
1	G	154	GLU	3.5
1	D	253	GLN	3.5
1	E	166	LYS	3.4
1	D	152	LYS	3.4
1	J	357	GLN	3.4
1	D	358	ASP	3.3
1	C	29	GLY	3.3
1	B	158	THR	3.3
1	E	165	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	318	HIS	3.3
1	B	191	LEU	3.3
1	B	194	SER	3.2
1	E	172	TYR	3.2
1	E	186	LEU	3.2
1	J	389	GLY	3.2
1	E	349	TYR	3.2
1	F	152	LYS	3.2
1	D	154	GLU	3.2
1	D	157	ARG	3.2
1	D	368	TYR	3.2
1	B	165	SER	3.1
1	B	184	TRP	3.1
1	B	187	ASP	3.1
1	I	154	GLU	3.1
1	J	355	ALA	3.1
1	B	154	GLU	3.0
1	C	28	LYS	3.0
1	D	247	ALA	3.0
1	B	185	GLY	3.0
1	A	153	VAL	3.0
1	F	153	VAL	3.0
1	J	30	PHE	3.0
1	D	355	ALA	3.0
1	B	339	ARG	3.0
1	J	318	HIS	3.0
1	B	151	GLU	3.0
1	B	164	VAL	3.0
1	F	356	ALA	3.0
1	B	199	VAL	2.9
1	E	356	ALA	2.9
1	I	152	LYS	2.9
1	B	358	ASP	2.9
1	D	194	SER	2.9
1	D	261	VAL	2.9
1	J	352	LEU	2.9
1	D	337	VAL	2.9
1	D	371	TYR	2.9
1	J	285	ASP	2.9
1	D	193	ALA	2.9
1	D	161	ASP	2.9
1	D	250	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	181	ARG	2.8
1	D	167	VAL	2.8
1	B	180	THR	2.8
1	C	163	VAL	2.8
1	J	32	TYR	2.8
1	E	351	ALA	2.7
1	D	346	TYR	2.7
1	B	389	GLY	2.7
1	H	28	LYS	2.7
1	H	316	ARG	2.7
1	J	351	ALA	2.7
1	C	30	PHE	2.7
1	D	255	MET	2.7
1	E	169	ARG	2.7
1	G	271	LYS	2.7
1	B	166	LYS	2.7
1	F	155	GLN	2.7
1	J	255	MET	2.7
1	D	195	VAL	2.6
1	J	252	PHE	2.6
1	H	390	GLN	2.6
1	D	252	PHE	2.6
1	D	362	VAL	2.6
1	F	357	GLN	2.6
1	H	388	GLN	2.6
1	E	352	LEU	2.6
1	B	337	VAL	2.5
1	J	361	PHE	2.5
1	G	155	GLN	2.5
1	D	285	ASP	2.5
1	F	247	ALA	2.5
1	J	354	ASP	2.5
1	B	146	PHE	2.5
1	J	256	ILE	2.5
1	B	169	ARG	2.5
1	E	268	CYS	2.4
1	F	254	HIS	2.4
1	D	54	ARG	2.4
1	B	357	GLN	2.4
1	J	272	LEU	2.4
1	B	193	ALA	2.4
1	D	353	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	356	ALA	2.4
1	I	153	VAL	2.4
1	J	388	GLN	2.4
1	C	357	GLN	2.3
1	C	254	HIS	2.3
1	D	266	ASP	2.3
1	E	346	TYR	2.3
1	C	389	GLY	2.3
1	A	157[A]	ARG	2.3
1	B	318	HIS	2.3
1	B	338	PRO	2.3
1	E	167	VAL	2.3
1	J	348	LYS	2.3
1	D	192	ASP	2.3
1	A	318	HIS	2.3
1	E	355	ALA	2.3
1	G	156	VAL	2.3
1	I	162	VAL	2.3
1	J	261	VAL	2.3
1	B	386	ARG	2.3
1	C	157	ARG	2.3
1	A	357	GLN	2.3
1	B	385	ARG	2.3
1	J	264	PHE	2.3
1	H	154	GLU	2.3
1	D	155	GLN	2.2
1	E	261	VAL	2.2
1	H	286	THR	2.2
1	J	29	GLY	2.2
1	E	348	LYS	2.2
1	E	161	ASP	2.2
1	A	154	GLU	2.2
1	E	267	PHE	2.2
1	D	335	TYR	2.2
1	J	265	PHE	2.2
1	J	345	LEU	2.2
1	C	285	ASP	2.2
1	F	285	ASP	2.2
1	E	177	ARG	2.2
1	G	163	VAL	2.2
1	B	160	GLU	2.2
1	I	357	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	384	PHE	2.2
1	J	254	HIS	2.1
1	D	248	ASP	2.1
1	B	150	ALA	2.1
1	J	287	GLU	2.1
1	B	149	VAL	2.1
1	E	173	ASN	2.1
1	A	155	GLN	2.1
1	G	157	ARG	2.1
1	J	349	TYR	2.1
1	E	360	THR	2.1
1	E	164	VAL	2.1
1	E	316	ARG	2.1
1	D	186	LEU	2.1
1	J	360	THR	2.1
1	J	353	ALA	2.1
1	C	54	ARG	2.1
1	D	159	SER	2.1
1	B	192	ASP	2.0
1	H	285	ASP	2.0
1	J	53	GLN	2.0
1	D	166	LYS	2.0
1	F	248	ASP	2.0
1	I	318	HIS	2.0
1	J	359	VAL	2.0
1	E	162	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	GOL	I	398	6/6	0.92	0.23	11.78	41,50,55,56	0
4	GOL	E	398	6/6	0.80	0.37	9.23	61,64,71,72	0
4	GOL	B	398	6/6	0.64	0.28	7.69	52,58,59,59	0
6	XYL	F	399	10/10	0.66	0.47	7.46	20,20,20,20	0
4	GOL	H	398	6/6	0.83	0.19	7.28	50,55,61,62	0
4	GOL	G	399	6/6	0.83	0.21	5.82	54,57,63,64	0
4	GOL	J	400	6/6	0.54	0.33	5.02	56,62,70,72	0
6	XYL	I	401	10/10	0.71	0.25	4.03	62,67,73,76	0
4	GOL	F	400	6/6	0.75	0.27	3.74	59,65,67,69	0
4	GOL	F	398	6/6	0.75	0.28	3.37	48,55,60,62	0
4	GOL	C	398	6/6	0.87	0.23	3.14	51,55,57,60	0
4	GOL	J	399	6/6	0.77	0.28	2.89	46,60,64,69	0
4	GOL	A	398	6/6	0.82	0.26	2.17	51,56,64,66	0
4	GOL	I	399	6/6	0.86	0.20	1.68	55,64,67,73	0
4	GOL	E	400	6/6	0.75	0.21	1.28	61,66,73,76	0
4	GOL	D	398	6/6	0.87	0.15	0.77	47,52,61,65	0
3	UDP	E	500	21/25	0.90	0.18	0.33	57,63,72,76	0
3	UDP	B	500	25/25	0.92	0.32	0.33	60,80,102,117	0
3	UDP	A	500	25/25	0.95	0.17	0.26	39,46,72,90	0
4	GOL	G	398	6/6	0.91	0.14	0.22	51,52,57,61	0
2	FAD	C	450	53/53	0.97	0.17	-0.04	39,48,61,70	0
2	FAD	G	450	53/53	0.96	0.16	-0.06	46,54,65,67	0
3	UDP	J	500	25/25	0.95	0.15	-0.09	38,47,85,108	0
3	UDP	I	500	21/25	0.96	0.17	-0.12	48,50,63,69	0
5	URM	D	600	36/36	0.95	0.20	-0.14	54,63,76,85	0
3	UDP	H	500	25/25	0.95	0.16	-0.16	41,48,73,90	0
2	FAD	I	450	53/53	0.97	0.15	-0.18	38,45,56,62	0
2	FAD	B	450	53/53	0.97	0.17	-0.32	35,47,62,66	0
3	UDP	G	500	25/25	0.94	0.16	-0.40	52,59,87,108	0
2	FAD	F	450	53/53	0.96	0.17	-0.43	40,47,54,60	0
2	FAD	D	450	53/53	0.96	0.16	-0.56	50,57,65,66	0
2	FAD	E	450	53/53	0.96	0.16	-0.56	45,60,70,74	0
3	UDP	F	500	25/25	0.94	0.16	-0.57	47,52,90,107	0
2	FAD	A	450	53/53	0.97	0.14	-0.58	38,46,51,55	0
2	FAD	H	450	53/53	0.97	0.15	-0.77	38,48,52,56	0
3	UDP	C	500	25/25	0.96	0.14	-0.85	50,58,85,108	0
2	FAD	J	450	53/53	0.96	0.15	-0.91	44,57,64,65	0
4	GOL	H	399	6/6	0.76	0.26	-	60,72,75,81	0
4	GOL	G	400	6/6	0.75	0.32	-	63,68,72,76	0
4	GOL	C	399	6/6	0.82	0.18	-	65,72,77,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	GOL	D	399	6/6	0.81	0.38	-	73,75,76,77	0
4	GOL	E	401	6/6	0.77	0.27	-	67,73,74,78	0
4	GOL	I	402	6/6	0.64	0.32	-	61,62,68,74	0
4	GOL	A	400	6/6	0.87	0.43	-	58,63,69,70	0
4	GOL	I	400	6/6	0.71	0.39	-	67,76,80,80	0
4	GOL	E	399	6/6	0.78	0.21	-	60,65,74,76	0
4	GOL	A	399	6/6	0.74	0.22	-	58,62,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.